



Australian Government

Patent Office  
Canberra

REC'D 22 JUN 2004

WIPO

PCT

I, LEANNE MYNOTT, MANAGER EXAMINATION SUPPORT AND SALES hereby certify that annexed is a true copy of the Provisional specification in connection with Application No. 2004901259 for a patent by AGRESEARCH LIMITED and AGRICULTURAL VICTORIA SERVICES PTY LTD as filed on 10 March 2004.

WITNESS my hand this  
Eleventh day of June 2004

LEANNE MYNOTT  
MANAGER EXAMINATION SUPPORT  
AND SALES



**PRIORITY  
DOCUMENT**

SUBMITTED OR TRANSMITTED IN  
COMPLIANCE WITH RULE 17.1(a) OR (b)

AUSTRALIA

*Patents Act 1990*

# PROVISIONAL SPECIFICATION

Invention Title: **Manipulation of organic acid biosynthesis and secretion 2**

The invention is described in the following statement:

## MANIPULATION OF ORGANIC ACID BIOSYNTHESIS AND SECRETION 2

The present invention relates to nucleic acid fragments encoding amino acid sequences for organic acid biosynthetic enzymes in plants, and the use thereof for the modification of organic acid biosynthesis and secretion in plants.

- 5 Documents cited in this specification are for reference purposes only and their inclusion is not acknowledgment that they form part of the common general knowledge in the relevant art.

Organic acids, such as citrate and malate, are key metabolites in plants. They are involved in numerous processes, including C4 and Crassulacean acid 10 metabolism (CAM) photosynthesis, stomatal and pulvinal movement, nutrient uptake, respiration, nitrogen assimilation, fatty acid oxidation, and providing energy to bacteroids in root nodules. For example, malate plays a key role in root nodule metabolism and nitrogen fixation, serving as the primary carbon source for bacteroid maintenance and nitrogenase activity, and is also tightly linked to nodule 15 nitrogen assimilation. Furthermore, the complexing role of organic acids produced and excreted from plant roots has also been associated with tolerance to the aluminium cation  $\text{Al}^{3+}$  which is toxic to many plants at micromolar concentrations. Aluminium toxicity has been recognized as a major limiting factor of plant 20 productivity on acidic soils, which account for approximately 40% of the earth's arable land.

The tricarboxylic acid cycle (TCA), also known as Krebs cycle (after its discoverer Hans Krebs) or citric acid cycle, moves electrons from organic acids to the oxidized redox cofactors  $\text{NAD}^+$  and FAD, forming NADH,  $\text{FADH}_2$ , and carbon dioxide ( $\text{CO}_2$ ). The reaction sequence of the TCA cycle involves: in a reaction 25 catalyzed by citrate synthase (CS), acetyl-CoA formed by the pyruvate dehydrogenase complex combines with oxaloacetate to produce the C<sub>6</sub> tricarboxylic acid, citrate. In the overall cycle, the citrate is oxidized to produce two molecules of  $\text{CO}_2$  in a series of reactions that leads to the formation of one oxaloacetate, three NADH, one  $\text{FADH}_2$ , and one ATP. The resulting oxaloacetate 30 reacts with another molecule of acetyl-CoA to continue the cycle. The oxidative decarboxylation of pyruvate yields an additional  $\text{CO}_2$  and NADH. Thus the TCA

cycle brings about the complete oxidation of pyruvate to three  $\text{CO}_2$  plus 10 electrons, which are stored temporarily as 4 NADH and 1  $\text{FADH}_2$ .

- Cytosolic reactions generate products that are transported into the mitochondria to feed the TCA cycle. The nature of the end product of the glycolytic
- 5 reactions in the cytosol of plants is determined by the relative activities of the three enzymes that can utilize phosphoenol-pyruvate (PEP) as substrate. Both pyruvate kinase and PEP-phosphatase form pyruvate; while PEP-carboxylase (PEPC) generates oxaloacetate. Pyruvate is transported directly into the mitochondrion. Oxaloacetate is either transported directly into the mitochondrion or first reduced
- 10 to malate by cytosolic malate dehydrogenase (MDH).

Before entering the TCA cycle proper, pyruvate is oxidised and decarboxylated by the pyruvate dehydrogenase enzyme complex to form  $\text{CO}_2$ , acetyl-CoA, and NADH. The pyruvate dehydrogenase enzyme complex, which requires the bound cofactors thiamine pyrophosphate, lipoic acid, and FAD as well

15 as free coenzyme A (CoASH) and  $\text{NAD}^+$ , links the TCA cycle to glycolysis.

It is known that the TCA cycle includes the following enzymes: pyruvate dehydrogenase, citrate synthase, citrate hydrolase, isocitrate dehydrogenase, oxoglutarate dehydrogenase, succinyl-CoA synthetase, succinate dehydrogenase, fumarase, malate dehydrogenase, NAD-malic enzyme and phosphoenolpyruvate

20 carboxylase.

In particular, citrate synthase (CS) catalyzes the condensation of acetyl-CoA and oxaloacetate to form the C6 molecule citrate and free CoASH, as the TCA cycle proper begins.

Malate dehydrogenase (MDH) catalyzes the final step of the TCA cycle,

25 oxidizing malate to oxaloacetate and producing NADH. This reaction catalyzed by MDH is reversible, thus allowing also for the reversible reduction of oxaloacetate to malate. The enzyme MDH is important in several metabolic pathways, and higher plants contain multiple forms that differ in co-enzyme specificity and subcellular localization. Chloroplasts contain an  $\text{NADP}^+$ -dependent MDH that

plays a critical role in balancing reducing equivalents between the cytosol and stroma. Plants also contain NAD-dependent MDHs which are found in a) mitochondria as part of the TCA cycle; b) cytosol and peroxisomes involved in malate-aspartate shuttles; and c) glyoxisomes functioning in  $\beta$ -oxidation. In root nodules of nitrogen-fixing legumes, such as white clover (*Trifolium repens*) and alfalfa (*Medicago sativa*), malate serves as the primary carbon source to support the respiratory needs of the bacterial microsymbiont and the fixation of N<sub>2</sub> by nitrogenase, and a nodule-enhanced MDH is thus critical for nodule function.

Phosphoenolpyruvate carboxylase (PEPC) catalyzes the reaction of phosphoenol-pyruvate with HCO<sub>3</sub><sup>-</sup> releasing the phosphate and producing the C<sub>4</sub> product, oxaloacetate. Oxaloacetate is commonly reduced to malate by NADH through the action of malata dehydrogenase (MDH). PEPC is a homotetrameric enzyme widely distributed in most plant tissues. In plants, PEPC fulfils various physiological roles such as the photosynthetic CO<sub>2</sub> fixation in C<sub>4</sub> and 15 Crassulacean Acid Metabolism (CAM) plants, and the anaplerotic pathway.

While nucleic acid sequences encoding some organic acid biosynthetic enzymes have been isolated for certain species of plants, there remains a need for materials useful in modifying organic acid biosynthesis; in modifying organic acid secretion; in modifying phosphorous acquisition efficiency in plants; in modifying 20 aluminium and acid soil tolerance in plants; in modifying nitrogen fixation and nodule function, particularly in forage legumes and grasses, including alfalfa, medics, clovers, ryegrasses and fescues, and for methods for their use.

This invention is directed towards overcoming, or at least alleviating, one or more of the difficulties or deficiencies associated with the prior art.

25 In one aspect, the present invention provides substantially purified or isolated nucleic acids or nucleic acid fragments encoding the organic acid biosynthetic enzymes CS, MDH and PEPC, from a clover (*Trifolium*), medic (*Medicago*), ryegrass (*Lolium*) or fescue (*Festuca*) species, or functionally active fragments or variants thereof.

The present invention also provides substantially purified or isolated nucleic acids or nucleic acid fragments encoding amino acid sequences for a class of proteins from a clover (*Trifolium*), medic (*Medicago*), ryegrass (*Lolium*) or fescue (*Festuca*) species which are related to CS, MDH and PEPC, or functionally active 5 fragments or variants thereof. Such proteins are referred to herein as CS-like, MDH-like and PEPC-like respectively.

The present invention also relates to individual or simultaneous enhancement or otherwise manipulation of CS, MDH and/or PEPC or like gene activities in plants to enhance or otherwise alter organic acid biosynthesis; to enhance or reduce or otherwise alter organic acid secretion; to enhance or reduce 10 or otherwise alter phosphorous acquisition efficiency in plants; to enhance or reduce or otherwise alter aluminium and acid soil tolerance in plants; and/or to enhance or reduce or otherwise alter nitrogen fixation and nodule function in legumes.

15 The individual or simultaneous enhancement or otherwise manipulation of CS, MDH and/or PEPC or like gene activities in plants has significant consequences for a range of applications in, for example, plant production, plant performance, plant nutrition and plant tolerance. For example, it has applications in increasing plant tolerance to aluminium-toxic acid soils; in improving plant 20 nutrient acquisition efficiency for example in increasing acquisition of phosphorus from soils; in increasing nodule function in nitrogen-fixing legumes for example leading to enhanced nitrogen fixation; in modifying the accumulation of organic acids such as citrate in fruits; in modifying the secretion of organic acids for example citrate and/or malate from plant roots.

25 Manipulation of CS, MDH and/or PEPC or like gene activities in plants, including legumes such as clovers (*Trifolium* species), lucerne (*Medicago sativa*) and grass species such as ryegrasses (*Lolium* species) and fescues (*Festuca* species) may be used to facilitate the production of, for example, forage legumes and forage grasses and other crops with enhanced tolerance to aluminium toxic 30 soils; enhanced nutrient acquisition efficiency; forage legumes with enhanced

nitrogen fixation; fruits with enhanced organic acid content leading to enhanced flavour and health benefits.

The clover (*Trifolium*), medic (*Medicago*), ryegrass (*Lolium*) or fescue (*Festuca*) species may be of any suitable type, including white clover (*Trifolium repens*), red clover (*Trifolium pratense*), subterranean clover (*Trifolium subterraneum*), alfalfa (*Medicago sativa*), Italian or annual ryegrass (*Lolium multiflorum*), perennial ryegrass (*Lolium perenne*), tall fescue (*Festuca arundinacea*), meadow fescue (*Festuca pratensis*) and red fescue (*Festuca rubra*). Preferably the species is a clover or a ryegrass, more preferably white clover (*T. repens*) or perennial ryegrass (*L. perenne*). White clover (*Trifolium repens L.*) and perennial ryegrass (*Lolium perenne L.*) are key pasture legumes and grasses, respectively, in temperate climates throughout the world. Perennial ryegrass is also an important turf grass.

The nucleic acid or nucleic acid fragment may be of any suitable type and includes DNA (such as cDNA or genomic DNA) and RNA (such as mRNA) that is single- or double-stranded, optionally containing synthetic, non-natural or altered nucleotide bases, and combinations thereof.

The term "isolated" means that the material is removed from its original environment (eg. the natural environment if it is naturally occurring). For example, a naturally occurring nucleic acid or polypeptide present in a living plant is not isolated, but the same nucleic acid or polypeptide separated from some or all of the coexisting materials in the natural system, is isolated. Such an isolated nucleic acid could be part of a vector and/or such a nucleic acid could be part of a composition, and still be isolated in that such a vector or composition is not part of its natural environment. An isolated polypeptide could be part of a composition and still be isolated in that such a composition is not part of its natural environment.

The term "purified" means that the nucleic acid or polypeptide is substantially free of other nucleic acids or polypeptides.

By "functionally active" in respect of a nucleotide sequence it is meant that the fragment or variant is capable of modifying organic acid biosynthesis in a plant. A variant in this context can be an analogue, derivative or mutant and includes naturally occurring allelic variants and non-naturally occurring variants. Additions,

- 5 deletions, substitutions and derivatizations of one or more of the nucleotides are contemplated so long as the modifications do not result in loss of functional activity of the fragment or variant. Preferably the functionally active fragment or variant has at least approximately 80% identity to the functional part of the above mentioned sequence, more preferably at least approximately 90% identity, most preferably at least approximately 95% identity. Such functionally active variants and fragments include, for example, those having nucleic acid changes which result in conservative amino acid substitutions of one or more residues in the corresponding amino acid sequence. Preferably the fragment has a size of at least 30 nucleotides, more preferably at least 45 nucleotides, most preferably at least 60
- 10 nucleotides.
- 15

By "functionally active" in the context of a polypeptide it is meant that the fragment or variant has one or more of the biological properties of the proteins CS, CS-like, MDH, MDH-like, PEPC and PEPC-like. A variant in this context includes additions, deletions, substitutions and derivatizations of one or more of the amino acids are contemplated so long as the modifications do not result in loss of functional activity of the fragment or variant. Preferably the functionally active fragment or variant has at least approximately 60% identity to the functional part of the above mentioned sequence, more preferably at least approximately 80% identity, most preferably at least approximately 90% identity. Such functionally active variants and fragments include, for example, those having conservative amino acid substitutions of one or more residues in the corresponding amino acid sequence. Preferably the fragment has a size of at least 10 amino acids, more preferably at least 15 amino acids, most preferably at least 20 amino acids.

- The term "construct" as used herein refers to an artificially assembled or
- 30 isolated nucleic acid molecule which includes the gene or genes of interest. In general a construct may include the gene or genes of interest, a marker gene which in some cases can also be the gene of interest and appropriate regulatory

sequences. It should be appreciated that the inclusion of regulatory sequences in a construct is optional, for example, such sequences may not be required in situations where the regulatory sequences of a host cell are to be used. The term construct includes vectors but should not be seen as being limited thereto.

- 5        The term "vector" as used herein encompasses both cloning and expression vectors. Vectors are often recombinant molecules containing nucleic acid molecules from several sources.

By "operatively linked" in respect of one or more regulatory elements, nucleic acids or nucleic acid fragments and terminators, is meant that said regulatory element(s) is capable of causing expression of said nucleic acid(s) or nucleic acid fragment(s) in a plant cell and said terminator(s) is capable of terminating expression of said nucleic acid(s) or nucleic acid fragment(s) in a plant cell. Preferably, said regulatory element(s) is upstream of said nucleic acid(s) or nucleic acid fragment(s) and said terminator(s) is downstream of said nucleic acid(s) or nucleic acid fragment(s).

In a particularly preferred embodiment, each nucleic acid or nucleic acid fragment has one or more upstream promoters and one or more downstream terminators, although expression of more than one nucleic acid or nucleic acid fragment from an upstream regulatory element(s) or termination of more than one nucleic acid or nucleic acid fragment from a downstream terminator(s) is not precluded.

By "an effective amount" of a nucleic acid or nucleic acid fragment it is meant an amount sufficient to result in an identifiable phenotypic trait in said plant, or a plant, plant seed or other plant part derived therefrom. Such amounts can be readily determined by an appropriately skilled person, taking into account the type of plant, the route of administration and other relevant factors. Such a person will readily be able to determine a suitable amount and method of administration. See, for example, Maniatis et al, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, Cold Spring Harbor, the entire disclosure of which is incorporated herein by reference.

It will also be understood that the term "comprises" (or its grammatical variants) as used in this specification is equivalent to the term "includes" and should not be taken as excluding the presence of other elements or features.

Such nucleic acids or nucleic acid fragments could be assembled to form a  
5 consensus contig. As used herein, the term "consensus contig" refers to a nucleotide sequence that is assembled from two or more constituent nucleotide sequences that share common or overlapping regions of sequence homology. For example, the nucleotide sequence of two or more nucleic acids or nucleic acid fragments can be compared and aligned in order to identify common or  
10 overlapping sequences. Where common or overlapping sequences exist between two or more nucleic acids or nucleic acid fragments, the sequences (and thus their corresponding nucleic acids or nucleic acid fragments) can be assembled into a single contiguous nucleotide sequence.

In a preferred embodiment of this aspect of the invention, the substantially purified or isolated nucleic acid or nucleic acid fragment encoding an CS or CS-like protein includes a nucleotide sequence selected from the group consisting of  
15 (a) sequences shown in Figures 1, 3, 4, 6, 7, 9, 99, 101, 102 and 104 hereto; (b) complements of the sequences shown in Figures 1, 3, 4, 6, 7, 9, 99, 101, 102 and 104 hereto; (c) sequences antisense to the sequences recited in (a) and (b); and  
20 (d) functionally active fragments and variants of the sequences recited in (a), (b) and (c).

In a further preferred embodiment of this aspect of the invention, the substantially purified or isolated nucleic acid or nucleic acid fragment encoding a MDH or MDH-like protein includes a nucleotide sequence selected from the group  
25 consisting of (a) sequences shown in Figures 11, 13, 14, 16, 17, 19, 21, 23, 25, 26, 28, 30, 31, 33, 35, 37, 38, 40, 50, 55, 57, 58, 60, 61, 63, 64, 66, 67, 69, 70, 72, 73, 75, 76, 78, 79, 81, 82 and 84 hereto; (b) complements of the sequences shown in Figures 11, 13, 14, 16, 17, 19, 21, 23, 25, 26, 28, 30, 31, 33, 35, 37, 38, 40, 50, 55, 57, 58, 60, 61, 63, 64, 66, 67, 69, 70, 72, 73, 75, 76, 78, 79, 81, 82 and  
30 84 hereto; (c) sequences antisense to the sequences recited in (a) and (b); and (d)

functionally active fragments and variants of the sequences recited in (a), (b) and (c).

In a further preferred embodiment of this aspect of the invention, the substantially purified or isolated nucleic acid or nucleic acid fragment encoding an

- 5 PEPC or PEPC-like protein includes a nucleotide sequence selected from the group consisting of (a) sequences shown in Figures 42, 44, 46, 47, 49, 51, 53, 86, 88, 89, 91, 92, 94, 95 and 97 hereto; (b) complements of the sequences shown in Figures 42, 44, 46, 47, 49, 51, 53, 86, 88, 89, 91, 92, 94, 95 and 97 hereto; (c) sequences antisense to the sequences recited in (a) and (b); and (d) functionally  
10 active fragments and variants of the sequences recited in (a), (b) and (c).

Genes encoding other CS or CS-like, MDH or MDH-like and PEPC or PEPC-like proteins, either as cDNAs or genomic DNAs, may be isolated directly by using all or a portion of the nucleic acids or nucleic acid fragments of the present invention as hybridisation probes to screen libraries from the desired plant

- 15 employing the methodology well known to those skilled in the art. Specific oligonucleotide probes based upon the nucleic acid sequences of the present invention may be designed and synthesized by methods known in the art. Moreover, the entire sequences may be used directly to synthesize DNA probes by methods known to the skilled artisan such as random primer DNA labelling,  
20 nick translation, or end-labelling techniques, or RNA probes using available *in vitro* transcription systems. In addition, specific primers may be designed and used to amplify a part or all of the sequences of the present invention. The resulting amplification products may be labelled directly during amplification reactions or labelled after amplification reactions, and used as probes to isolate full-length  
25 cDNA or genomic fragments under conditions of appropriate stringency.

In addition, short segments of the nucleic acids or nucleic acid fragments of the present invention may be used in protocols to amplify longer nucleic acids or nucleic acid fragments encoding homologous genes from DNA or RNA. For example, polymerase chain reaction may be performed on a library of cloned

- 30 nucleic acid fragments wherein the sequence of one primer is derived from the nucleic acid sequences of the present invention, and the sequence of the other

- primer takes advantage of the presence of the polyadenylic acid tracts to the 3' end of the mRNA precursor encoding plant genes. Alternatively, the second primer sequence may be based upon sequences derived from the cloning vector. For example, those skilled in the art can follow the RACE protocol (Frohman *et al.*
- 5 (1988) *Proc. Natl. Acad. Sci. USA* 85:8998, the entire disclosure of which is incorporated herein by reference) to generate cDNAs by using PCR to amplify copies of the region between a single point in the transcript and the 3' or 5' end. Using commercially available 3' RACE and 5' RACE systems (BRL), specific 3' or 5' cDNA fragments may be isolated (Ohara *et al.* (1989) *Proc. Natl. Acad. Sci USA*
- 10 86:5673; Loh *et al.* (1989) *Science* 243:217, the entire disclosures of which are incorporated herein by reference). Products generated by the 3' and 5' RACE procedures may be combined to generate full-length cDNAs.

In a further aspect of the present invention there is provided a substantially purified or isolated polypeptide from a clover (*Trifolium*), medic (*Medicago*), ryegrass (*Lolium*) or fescue (*Festuca*) species, selected from the group consisting of CS or CS-like, MDH or MDH-like and PEPC or PEPC-like proteins; and functionally active fragments and variants thereof.

The clover (*Trifolium*), medic (*Medicago*), ryegrass (*Lolium*) or fescue (*Festuca*) species may be of any suitable type, including white clover (*Trifolium repens*), red clover (*Trifolium pratense*), subterranean clover (*Trifolium subterraneum*), alfalfa (*Medicago sativa*), Italian or annual ryegrass (*Lolium multiflorum*), perennial ryegrass (*Lolium perenne*), tall fescue (*Festuca arundinacea*), meadow fescue (*Festuca pratensis*) and red fescue (*Festuca rubra*). Preferably the species is a clover or a ryegrass, more preferably white clover (*T. repens*) or perennial ryegrass (*L. perenne*).

In a preferred embodiment of this aspect of the invention, the substantially purified or isolated CS or CS-like polypeptide includes an amino acid sequence selected from the group consisting of the sequences shown in Figures 2, 5, 8, 10, 100 and 103 hereto, and functionally active fragments and variants thereof.

In a further preferred embodiment of this aspect of the invention, the substantially purified or isolated MDH or MDH-like polypeptide includes an amino acid sequence selected from the group consisting of the sequences shown in Figures 12, 15, 18, 20, 22, 24, 27, 29, 32, 34, 36, 39, 41, 56, 59, 62, 65, 68, 71, 5 74, 77, 80, 83 and 85 hereto, and functionally active fragments and variants thereof.

In a further preferred embodiment of this aspect of the invention, the substantially purified or isolated PEPC or PEPC-like polypeptide includes an amino acid sequence selected from the group consisting of the sequences shown 10 in Figures 43, 45, 48, 50, 52, 54, 87, 90, 93, 96 and 98 hereto, and functionally active fragments and variants thereof.

In a further embodiment of this aspect of the invention, there is provided a polypeptide recombinantly produced from a nucleic acid or nucleic acid fragment according to the present invention. Techniques for recombinantly producing 15 polypeptides are known to those skilled in the art.

Availability of the nucleotide sequences of the present invention and deduced amino acid sequences facilitates immunological screening of cDNA expression libraries. Synthetic peptides representing portions of the instant amino acid sequences may be synthesized. These peptides may be used to immunise 20 animals to produce polyclonal or monoclonal antibodies with specificity for peptides and/or proteins including the amino acid sequences. These antibodies may be then used to screen cDNA expression libraries to isolate full-length cDNA clones of interest.

A genotype is the genetic constitution of an individual or group. Variations in 25 genotype are important in commercial breeding programs, in determining parentage, in diagnostics and fingerprinting, and the like. Genotypes can be readily described in terms of genetic markers. A genetic marker identifies a specific region or locus in the genome. The more genetic markers, the finer defined is the genotype. A genetic marker becomes particularly useful when it is 30 allelic between organisms because it then may serve to unambiguously identify an

individual. Furthermore, a genetic marker becomes particularly useful when it is based on nucleic acid sequence information that can unambiguously establish a genotype of an individual and when the function encoded by such nucleic acid is known and is associated with a specific trait. Such nucleic acids and/or nucleotide sequence information including single nucleotide polymorphisms (SNPs), variations in single nucleotides between allelic forms of such nucleotide sequence, may be used as perfect markers or candidate genes for the given trait.

Applicants have identified a number of SNPs of the nucleic acids or nucleic acid fragments of the present invention. These are indicated (marked with grey on the black background) in the figures that show multiple alignments of nucleotide sequences of nucleic acid fragments contributing to consensus contig sequences. See for example, Figures 3, 6, 13, 16, 25, 30, 37, 46, 57, 60, 63, 66, 69, 72, 75, 78, 81, 88, 91, 94 101 and 104 hereto.

Accordingly, in a further aspect of the present invention, there is provided a substantially purified or isolated nucleic acid or nucleic acid fragment including a single nucleotide polymorphism (SNP) from a nucleic acid or nucleic acid fragment according to the present invention, for example a SNP from a nucleic acid sequence shown in Figures 3, 6, 13, 16, 25, 30, 37, 46, 57, 60, 63, 66, 69, 72, 75, 78, 81, 88, 91, 94, 101 and 104 hereto; or complements or sequences antisense thereto, and functionally active fragments and variants thereof. The invention further provides a substantially purified or isolated nucleic acid or nucleic acid fragment including a single nucleotide polymorphism (SNP) isolated by the method of this invention.

In a still further aspect of the present invention there is provided a method of isolating a nucleic acid or nucleic acid fragment of the present invention including a SNP, said method including sequencing nucleic acid fragments from a nucleic acid library. The method includes the step of identifying the SNP.

The nucleic acid library may be of any suitable type and is preferably a cDNA library.

The nucleic acid or nucleic acid fragment may be isolated from a recombinant plasmid or may be amplified, for example using polymerase chain reaction.

The sequencing may be performed by techniques known to those skilled in  
5 the art.

In a still further aspect of the present invention, there is provided use of the nucleic acids or nucleic acid fragments of the present invention including SNPs, and/or nucleotide sequence information thereof, as molecular genetic markers.

In a still further aspect of the present invention there is provided use of a  
10 nucleic acid or nucleic acid fragment of the present invention, and/or nucleotide sequence information thereof, as a molecular genetic marker.

More particularly, nucleic acids or nucleic acid fragments according to the present invention and/or nucleotide sequence information thereof may be used as a molecular genetic marker for quantitative trait loci (QTL) tagging, QTL mapping,  
15 DNA fingerprinting and in marker assisted selection, particularly in clovers, alfalfa, ryegrasses and fescues. Even more particularly, nucleic acids or nucleic acid fragments according to the present invention and/or nucleotide sequence information thereof may be used as molecular genetic markers in plant improvement in relation to plant tolerance to abiotic stresses such aluminium toxic  
20 acid soils; in relation to nutrient acquisition efficiency including phosphorus; in relation to nitrogen fixation; in relation to nodulation. Even more particularly, sequence information revealing SNPs in allelic variants of the nucleic acids or nucleic acid fragments of the present invention and/or nucleotide sequence information thereof may be used as molecular genetic markers for QTL tagging  
25 and mapping and in marker assisted selection, particularly in clovers, alfalfa, ryegrasses and fescues.

In a still further aspect of the present invention there is provided a construct including one or more nucleic acids or nucleic acid fragments according to the present invention.

In a still further aspect of the present invention there is provided a vector including one or more nucleic acids or nucleic acid fragments according to the present invention.

In a preferred embodiment of this aspect of the invention, the vector may

- 5 include one or several of the following: one or more regulatory elements such as promoters, one or more nucleic acids or nucleic acid fragments according to the present invention and one or more terminators; said one or more regulatory elements, one or more nucleic acids or nucleic acid fragments and one or more terminators being operatively linked.

10 In a preferred embodiment of the present invention the vector may contain nucleic acids or nucleic acid fragments encoding both CS or CS-like and MDH or MDH-like polypeptides, operatively linked to a regulatory element or regulatory elements, such that both CS or CS-like and MDH or MDH-like proteins are expressed.

15 In another preferred embodiment of the present invention the vector may contain nucleic acids or nucleic acid fragments encoding both CS or CS-like and PEPC or PEPC-like polypeptides, operatively linked to a regulatory element or regulatory elements, such that both CS or CS-like and PEPC or PEPC-like proteins are expressed.

20 In yet another particularly preferred embodiment of the present invention the vector may contain nucleic acids or nucleic acid fragments encoding both MDH or MDH-like and PEPC or PEPC-like polypeptides, operatively linked to a regulatory element or regulatory elements, such that both MDH or MDH-like and PEPC or PEPC-like proteins are expressed.

25 In another particularly preferred embodiment of the present invention the vector may contain nucleic acids or nucleic acid fragments encoding all three of CS or CS-like, MDH or MDH-like and PEPC or PEPC-like, operatively linked to a regulatory element or regulatory elements, such that all three of CS or CS-like, MDH or MDH-like and PEPC or PEPC-like proteins are expressed.

The vector may be of any suitable type and may be viral or non-viral. The vector may be an expression vector. Such vectors include chromosomal, non-chromosomal and synthetic nucleic acid sequences, eg. derivatives of plant viruses; bacterial plasmids; derivatives of the Ti plasmid from *Agrobacterium tumefaciens*, derivatives of the Ri plasmid from *Agrobacterium rhizogenes*; phage DNA; yeast artificial chromosomes; bacterial artificial chromosomes; binary bacterial artificial chromosomes; vectors derived from combinations of plasmids and phage DNA. However, any other vector may be used as long as it is replicable, integrative or viable in the plant cell.

10 The regulatory element and terminator may be of any suitable type and may be endogenous to the target plant cell or may be exogenous, provided that they are functional in the target plant cell.

Preferably the regulatory element is a promoter. A variety of promoters which may be employed in the vectors of the present invention are well known to those skilled in the art. Factors influencing the choice of promoter include the desired tissue specificity of the vector, and whether constitutive or inducible expression is desired and the nature of the plant cell to be transformed (eg. monocotyledon or dicotyledon). Particularly suitable constitutive promoters include the Cauliflower Mosaic Virus 35S (CaMV 35S) promoter, the maize Ubiquitin promoter, and the rice Actin promoter. Particularly suitable tissue specific promoters include root prevalent promoters.

A variety of terminators which may be employed in the vectors of the present invention are also well known to those skilled in the art. The terminator may be from the same gene as the promoter sequence or a different gene. 25 Particularly suitable terminators are polyadenylation signals, such as the CaMV 35S polyA and other terminators from the nopaline synthase (*nos*) and the octopine synthase (*ocs*) genes.

The vector, in addition to the regulatory element(s), the nucleic acid(s) or nucleic acid fragment(s) of the present invention and the terminator(s), may 30 include further elements necessary for expression of the nucleic acid(s) or nucleic

acid fragment(s), in different combinations, for example vector backbone, origin of replication (ori), multiple cloning sites; spacer sequences, enhancers, introns (such as the maize Ubiquitin *Ubi* intron), antibiotic resistance genes and other selectable marker genes [such as the neomycin phosphotransferase (*npt2*) gene, the

- 5 hygromycin phosphotransferase (*hph*) gene, the phosphinothricin acetyltransferase (*bar* or *pat*) gene, the phospho-mannose isomerase (*pmi*) gene], and reporter genes (such as beta-glucuronidase (GUS) gene (*gusA*]). The vector may also contain a ribosome binding site for translation initiation. The vector may also include appropriate sequences for amplifying expression.

10 As an alternative to use of a selectable marker gene to provide a phenotypic trait for selection of transformed host cells, the presence of the vector in transformed cells may be determined by other techniques well known in the art, such as PCR (polymerase chain reaction), Southern blot hybridisation analysis, histochemical GUS assays, northern and Western blot hybridisation analyses.

- 15 Those skilled in the art will appreciate that the various components of the vector are operatively linked, so as to result in expression of said nucleic acid(s) or nucleic acid fragment(s). Techniques for operatively linking the components of the vector of the present invention are well known to those skilled in the art. Such techniques include the use of linkers, such as synthetic linkers, for example  
20 including one or more restriction enzyme sites.

The constructs and vectors of the present invention may be incorporated into a variety of plants, including monocotyledons (such as grasses from the genera *Lolium*, *Festuca*, *Paspalum*, *Pennisetum*, *Panicum* and other forage and turfgrasses, corn, oat, sugarcane, wheat and barley), dicotyledons (such as 25 *arabidopsis*, tobacco, clovers, medics, eucalyptus, potato, sugarbeet, canola, soybean, chickpea) and gymnosperms. In a preferred embodiment, the constructs and vectors may be used to transform monocotyledons, preferably grass species such as ryegrasses (*Lolium* species) and fescues (*Festuca* species), more 30 preferably perennial ryegrass, including forage- and turf-type cultivars. In an alternate preferred embodiment, the vectors may be used to transform dicotyledons, preferably forage legume species such as clovers (*Trifolium* species)

and medics (*Medicago* species), more preferably white clover (*Trifolium repens*), red clover (*Trifolium pratense*), subterranean clover (*Trifolium subterraneum*) and alfalfa (*Medicago sativa*). Clovers, alfalfa and medics are key pasture legumes in temperate climates throughout the world.

5        Techniques for incorporating the constructs and vectors of the present invention into plant cells (for example by transduction, transfection or transformation) are known to those skilled in the art. Such techniques include *Agrobacterium* mediated introduction, electroporation to tissues, cells and protoplasts, protoplast fusion, injection into reproductive organs, injection into  
10      immature embryos and high velocity projectile introduction to cells, tissues, calli, immature and mature embryos. The choice of technique will depend largely on the type of plant to be transformed.

Cells incorporating the constructs and vectors of the present invention may be selected, as described above, and then cultured in an appropriate medium to  
15      regenerate transformed plants, using techniques well known in the art. The culture conditions, such as temperature, pH and the like, will be apparent to the person skilled in the art. The resulting plants may be reproduced, either sexually or asexually, using methods well known in the art, to produce successive generations of transformed plants.

20       In a further aspect of the present invention there is provided a plant cell, plant, plant seed or other plant part, including, e.g. transformed with, one or more constructs, vectors, nucleic acids or nucleic acid fragments of the present invention.

The plant cell, plant, plant seed or other plant part may be from any suitable  
25      species, including monocotyledons, dicotyledons and gymnosperms. In a preferred embodiment the plant cell, plant, plant seed or other plant part may be from a monocotyledon, preferably a grass species, more preferably a ryegrass (*Lolium* species) or fescue (*Festuca* species), more preferably perennial ryegrass, including both forage- and turf-type cultivars. In an alternate preferred embodiment  
30      the plant cell, plant, plant seed or other plant part may be from a dicotyledon,

preferably forage legume species such as clovers (*Trifolium* species) and medics (*Medicago* species), more preferably white clover (*Trifolium repens*), red clover (*Trifolium pratense*), subterranean clover (*Trifolium subterraneum*) and alfalfa (*Medicago sativa*).

- 5 The present invention also provides a plant, plant seed or other plant part, or a plant extract derived from a plant cell of the present invention.

The present invention also provides a plant, plant seed or other plant part, or a plant extract derived from a plant of the present invention.

- In a further aspect of the present invention there is provided a method of  
10 modifying organic acid biosynthesis; of modifying organic acid secretion; of  
modifying phosphorous and other nutrients acquisition efficiency in plants; of  
modifying aluminium and acid soil tolerance in plants; of modifying nitrogen  
fixation and nodule function, said method including introducing into said plant an  
effective amount of a nucleic acid or nucleic acid fragment, construct and/or vector  
15 according to the present invention.

Using the methods and products of the present invention, organic acid  
biosynthesis; organic acid secretion; phosphorous and other plant nutrient  
acquisition efficiency; aluminium and acid soil tolerance; nitrogen fixation and  
nodule function, may be increased or otherwise altered, for example by  
20 incorporating additional copies of one or more sense nucleic acids or nucleic acid  
fragments of the present invention. They may be decreased or otherwise altered,  
for example by incorporating one or more antisense nucleic acids or nucleic acid  
fragments of the present invention.

- The present invention will now be more fully described with reference to the  
25 accompanying Examples and drawings. It should be understood, however, that the  
description following is illustrative only and should not be taken in any way as a  
restriction on the generality of the invention described above.

In the Figures

Figure 1 shows the consensus contig nucleotide sequence of LpCSa.

Figure 2 shows the deduced amino acid sequence of LpCSa.

Figure 3 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence LpCSa.

5       Figure 4 shows the consensus contig nucleotide sequence of LpCSb.

Figure 5 shows the deduced amino acid sequence of LpCSb.

Figure 6 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence LpCSb.

Figure 7 shows the nucleotide sequence of LpCSc.

10      Figure 8 shows the deduced amino acid sequence of LpCSc.

Figure 9 shows the nucleotide sequence of LpCSD.

Figure 10 shows the deduced amino acid sequence of LpCSD.

Figure 11 shows the consensus contig nucleotide sequence of LpMDHa.

Figure 12 shows the deduced amino acid sequence of LpMDHa.

15      Figure 13 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence LpMDHa.

Figure 14 shows the consensus contig nucleotide sequence of LpMDHb.

Figure 15 shows the deduced amino acid sequence of LpMDHb.

20      Figure 16 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence LpMDHb.

Figure 17 shows the nucleotide sequence of LpMDHc.

Figure 18 shows the deduced amino acid sequence of LpMDHc.

Figure 19 shows the nucleotide sequence of LpMDHd.

Figure 20 shows the deduced amino acid sequence of LpMDHd.

25      Figure 21 shows the nucleotide sequence of LpMDHe.

Figure 22 shows the deduced amino acid sequence of LpMDHe.

Figure 23 shows the consensus contig nucleotide sequence of LpMDHf.

Figure 24 shows the deduced amino acid sequence of LpMDHf.

Figure 25 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence LpMDHf.

Figure 26 shows the nucleotide sequence of LpMDHg.

5      Figure 27 shows the deduced amino acid sequence of LpMDHg.

Figure 28 shows the consensus contig nucleotide sequence of LpMDHh.

Figure 29 shows the deduced amino acid sequence of LpMDHh.

Figure 30 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence LpMDHh.

10     Figure 31 shows the nucleotide sequence of LpMDHi.

Figure 32 shows the deduced amino acid sequence of LpMDHi.

Figure 33 shows the nucleotide sequence of LpMDHj.

Figure 34 shows the deduced amino acid sequence of LpMDHj.

Figure 35 shows the consensus contig nucleotide sequence of LpMDHk.

15     Figure 36 shows the deduced amino acid sequence of LpMDHk.

Figure 37 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence LpMDHk.

Figure 38 shows the nucleotide sequence of LpMDHl.

Figure 39 shows the deduced amino acid sequence of LpMDHl.

20     Figure 40 shows the nucleotide sequence of LpMDHm.

Figure 41 shows the deduced amino acid sequence of LpMDHm.

Figure 42 shows the nucleotide sequence of LpPEPCa.

Figure 43 shows the deduced amino acid sequence of LpPEPCa.

Figure 44 shows the consensus contig nucleotide sequence of LpPEPCb.

25     Figure 45 shows the deduced amino acid sequence of LpPEPCb.

Figure 46 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence LpPEPCb.

Figure 47 shows the nucleotide sequence of LpPEPCc.

Figure 48 shows the deduced amino acid sequence of LpPEPCc.

Figure 49 shows the nucleotide sequence of LpPEPCd.

Figure 50 shows the deduced amino acid sequence of LpPEPCd.

5       Figure 51 shows the nucleotide sequence of LpPEPCe.

Figure 52 shows the deduced amino acid sequence of LpPEPCe.

Figure 53 shows the nucleotide sequence of LpPEPCf.

Figure 54 shows the deduced amino acid sequence of LpPEPCf.

Figure 55 shows the consensus contig nucleotide sequence of TrMDHa.

10      Figure 56 shows the deduced amino acid sequence of TrMDHa.

Figure 57 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrMDHa.

Figure 58 shows the consensus contig nucleotide sequence of TrMDHb.

Figure 59 shows the deduced amino acid sequence of TrMDHb.

15      Figure 60 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrMDHb.

Figure 61 shows the consensus contig nucleotide sequence of TrMDHc.

Figure 62 shows the deduced amino acid sequence of TrMDHc.

20      Figure 63 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrMDHc.

Figure 64 shows the consensus contig nucleotide sequence of TrMDHd.

Figure 65 shows the deduced amino acid sequence of TrMDHd.

Figure 66 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrMDHd.

25      Figure 67 shows the consensus contig nucleotide sequence of TrMDHe.

Figure 68 shows the deduced amino acid sequence of TrMDHe.

Figure 69 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrMDHe.

Figure 70 shows the consensus contig nucleotide sequence of TrMDHf.

Figure 71 shows the deduced amino acid sequence of TrMDHf.

5 Figure 72 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrMDHf.

Figure 73 shows the consensus contig nucleotide sequence of TrMDHg.

Figure 74 shows the deduced amino acid sequence of TrMDHg.

10 Figure 75 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrMDHg.

Figure 76 shows the consensus contig nucleotide sequence of TrMDHh.

Figure 77 shows the deduced amino acid sequence of TrMDHh.

Figure 78 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrMDHh.

15 Figure 79 shows the consensus contig nucleotide sequence of TrMDHi.

Figure 80 shows the deduced amino acid sequence of TrMDHi.

Figure 81 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrMDHi.

Figure 82 shows the nucleotide sequence of TrMDHj.

20 Figure 83 shows the deduced amino acid sequence of TrMDHj.

Figure 84 shows the nucleotide sequence of TrMDHk.

Figure 85 shows the deduced amino acid sequence of TrMDHk.

Figure 86 shows the consensus contig nucleotide sequence of TrPEPCa.

Figure 87 shows the deduced amino acid sequence of TrPEPCa.

25 Figure 88 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrPEPCa.

Figure 89 shows the consensus contig nucleotide sequence of TrPEPCb.

Figure 90 shows the deduced amino acid sequence of TrPEPCb.

Figure 91 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrPEPCb.

Figure 92 shows the consensus contig nucleotide sequence of TrPEPCc.

Figure 93 shows the deduced amino acid sequence of TrPEPCc.

5       Figure 94 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrPEPCc.

Figure 95 shows the nucleotide sequence of TrPEPCd.

Figure 96 shows the deduced amino acid sequence of TrPEPCd.

Figure 97 shows the nucleotide sequence of TrPEPCe.

10      Figure 98 shows the deduced amino acid sequence of TrPEPCe.

Figure 99 shows the consensus contig nucleotide sequence of TrCSa.

Figure 100 shows the deduced amino acid sequence of TrCSa.

Figure 101 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrCSa.

15      Figure 102 shows the consensus contig nucleotide sequence of TrCSb.

Figure 103 shows the deduced amino acid sequence of TrCSb.

Figure 104 shows the nucleotide sequences of the nucleic acid fragments contributing to the consensus contig sequence TrCSb.

20

#### EXAMPLE 1

**Preparation of cDNA libraries, isolation and sequencing of cDNAs coding for CS, CS-like, MDH, MDH-like, PEPC and PEPC-like proteins from white clover (*Trifolium repens*) and perennial ryegrass (*Lolium perenne*)**

25      cDNA libraries representing mRNAs from various organs and tissues of white clover (*Trifolium repens*) and perennial ryegrass (*Lolium perenne*) were prepared. The characteristics of the white clover and perennial ryegrass libraries, respectively, are described below (Tables 1 and 2).

**TABLE 1**  
**cDNA libraries from white clover (*Trifolium repens*)**

Library	Organ/Tissue
01wc	Whole seedling, light grown
02wc	Nodulated root 3, 5, 10, 14, 21 & 28 day old seedling
03wc	Nodules pinched off roots of 42 day old rhizobium inoculated wc
04wc	Nodulated wc cut leaf and stem collected after 0, 1, 4, 6 & 14 h after cutting
05wc	Non-nodulated Inflorescences: <50% open, not fully open and fully open
06wc	Dark grown etiolated
07wc	Inflorescence – very early stages, stem elongation, < 15 petals, 15-20 petals
08wc	seed frozen at -80°C, imbibed in dark overnight at 10°C
09wc	Drought stressed plants
10wc	AMV infected leaf
11wc	WCMV infected leaf
12wc	Phosphorus starved plants
13wc	Vegetative stolon tip
14wc	stolon root initials
15wc	Senescing stolon
16wc	Senescing leaf

**TABLE 2**  
**cDNA libraries from perennial ryegrass (*Lolium perenne*)**

Library	Organ/Tissue
01rg	Roots from 3-4 day old light-grown seedlings
02rg	Leaves from 3-4 day old light-grown seedlings
03rg	Etiolated 3-4 day old dark-grown seedlings
04rg	Whole etiolated seedlings (1-5 day old and 17 days old)
05rg	Senescent leaves from mature plants
06rg	Whole etiolated seedlings (1-5 day old and 17 days old)
07rg	Roots from mature plants grown in hydroponic culture
08rg	Senescent leaf tissue
09rg	Whole tillers and sliced leaves (0, 1, 3, 6, 12 and 24 h after harvesting)
10rg	Embryogenic suspension-cultured cells
11rg	Non-embryogenic suspension-cultured cells
12rg	Whole tillers and sliced leaves (0, 1, 3, 6, 12 and 24 h after harvesting)
13rg	Shoot apices including vegetative apical meristems
14rg	Immature inflorescences including different stages of inflorescence meristem and inflorescence development
15rg	Defatted pollen
16rg	Leaf blades and leaf sheaths ( <i>rbcL</i> , <i>rbcS</i> , <i>cab</i> , <i>wir2A</i> subtracted)
17rg	Senescent leaves and tillers
18rg	Drought-stressed tillers (pseudostems from plants subjected to PEG-simulated drought stress)

Library	Organ/Tissue
19rg	Non-embryogenic suspension-cultured cells subjected to osmotic stress (grown in media with half-strength salts) (1, 2, 3, 4, 5, 6, 24 and 48 h after transfer)
20rg	Non-embryogenic suspension-cultured cells subjected to osmotic stress (grown in media with double-strength salts) (1, 2, 3, 4, 5, 6, 24 and 48 h after transfer)
21rg	Drought-stressed tillers (pseudostems from plants subjected to PEG-simulated drought stress)
22rg	Spikelets with open and maturing florets
23rg	Mature roots (specific subtraction with leaf tissue)

- The cDNA libraries may be prepared by any of many methods available. For example, total RNA may be isolated using the Trizol method (Gibco-BRL, USA) or the RNeasy Plant Mini kit (Qiagen, Germany), following the manufacturers' instructions. cDNAs may be generated using the SMART PCR cDNA synthesis kit (Clontech, USA), cDNAs may be amplified by long distance polymerase chain reaction using the Advantage 2 PCR Enzyme system (Clontech, USA), cDNAs may be cleaned using the GeneClean spin column (Bio 101, USA), tailed and size fractionated, according to the protocol provided by Clontech. The cDNAs may be introduced into the pGEM-T Easy Vector system 1 (Promega, USA) according to the protocol provided by Promega. The cDNAs in the pGEM-T Easy plasmid vector are transfected into *Escherichia coli* Epicurian coli XL10-Gold ultra competent cells (Stratagene, USA) according to the protocol provided by Stratagene.
- Alternatively, the cDNAs may be introduced into plasmid vectors for first preparing the cDNA libraries in Uni-ZAP XR vectors according to the manufacturer's protocol (Stratagene Cloning Systems, La Jolla, CA, USA). The Uni-ZAP XR libraries are converted into plasmid libraries according to the protocol provided by Stratagene. Upon conversion, cDNA inserts will be contained in the

plasmid vector pBluescript. In addition, the cDNAs may be introduced directly into precut pBluescript II SK(+) vectors (Stratagene) using T4 DNA ligase (New England Biolabs), followed by transfection into *E. coli* DH10B cells according to the manufacturer's protocol (GIBCO BRL Products).

- 5 Once the cDNA inserts are in plasmid vectors, plasmid DNAs are prepared from randomly picked bacterial colonies containing recombinant plasmids, or the insert cDNA sequences are amplified via polymerase chain reaction using primers specific for vector sequences flanking the inserted cDNA sequences. Plasmid DNA preparation may be performed robotically using the Qiagen QiaPrep Turbo kit
- 10 (Qiagen, Germany) according to the protocol provided by Qiagen. Amplified insert DNAs are sequenced in dye-terminator sequencing reactions to generate partial cDNA sequences (expressed sequence tags or "ESTs"). The resulting ESTs are analyzed using an Applied Biosystems ABI 3700 sequence analyser.

#### EXAMPLE 2

##### 15 DNA sequence analyses

- The cDNA clones encoding CS, CS-like, MDH, MDH-like, PEPC and PEPC-like proteins were identified by conducting BLAST (Basic Local Alignment Search Tool; Altschul *et al.* (1993) *J. Mol. Biol.* 215:403-410) searches. The cDNA sequences obtained were analysed for similarity to all publicly available DNA sequences contained in the eBioinformatics nucleotide database using the BLASTN algorithm provided by the National Center for Biotechnology Information (NCBI). The DNA sequences were translated in all reading frames and compared for similarity to all publicly available protein sequences contained in the SWISS-PROT protein sequence database using BLASTx algorithm (v 2.0.1) (Gish and States (1993) *Nature Genetics* 3:266-272) provided by the NCBI.

- The cDNA sequences obtained and identified were then used to identify additional identical and/or overlapping cDNA sequences generated using the BLASTN algorithm. The identical and/or overlapping sequences were subjected to a multiple alignment using the CLUSTALw algorithm, and to generate a consensus 30 contig sequence derived from this multiple sequence alignment. The consensus contig sequence was then used as a query for a search against the SWISS-PROT

protein sequence database using the BLASTx algorithm to confirm the initial identification.

Finally, it is to be understood that various alterations, modifications and/or additions may be made without departing from the spirit of the present invention as  
5 outlined herein.

**Agriculture Victoria Services Pty Ltd**

**AgResearch Limited**

By their Registered Patent Attorneys

**Freehills Carter Smith Beadle**

10 March 2004

Figure 1 Consensus contig nucleotide sequence of LpCSa

LpCSa :	GNNTTATATTGACGGGGATGAGGGATTCTCGCTACAGAGGCTATCCAATTGAGGAGGT	:	60
	* 20 * 40 * 60		
LpCSa :	GGCTGAAAGCAGCTCGTTGAGGTCGCCTACCTCTTAATGTATGGGAATTGCCAC	:	120
	* 80 * 100 * 120		
LpCSa :	CCAGAGTCAACTGGCAGGCTGGGAGTTGCAATTTCGCAGCACTGCTGTTCTCAAGG	:	180
	* 140 * 160 * 180		
LpCSa :	ACTCTTGATATAATACAATCAATGCCTCATGATGCCACCCATGGGTGTCCTGCCAG	:	240
	* 200 * 220 * 240		
LpCSa :	TGCAATGAGCACACTTCAGTCTCCATCCAGATGCAAACCTGCTTAGAGGTCAAGA	:	300
	* 260 * 280 * 300		
LpCSa :	TCTATACAAGTCGAAGCAGGTTAGGGATAAGCAAATTGTACGAGTTGGGAAGGCACC	:	360
	* 320 * 340 * 360		
LpCSa :	AGTAATAGCAGCTGCAGCCTATCTGAGATTAGCAGGAAGGCCCTTGTCCCTTCAAA	:	420
	* 380 * 400 * 420		
LpCSa :	TAATCTCTTATTCAAGAAATTCTTGATATGCTGGACTCTATGGTGACAAAGATTA	:	480
	* 440 * 460 * 480		
LpCSa :	TAAGCCAAATCCCAGACTTGCCCCGGTTCTGGATGTCCTTTATTCTCATGCTGAACA	:	540
	* 500 * 520 * 540		
LpCSa :	CGAAATGAACTGCTAACAGCTGCTGTTAGGCACCTTGCTCAAGTGGTGTGATGTCTT	:	600
	* 560 * 580 * 600		
LpCSa :	CACTGCTCTCTGGTGCTGTTGGAGCTCTATATGGTCCACTGCATGGTGGCGCAAATGA	:	660
	* 620 * 640 * 660		
LpCSa :	GGCGGTACTAAAATGTTAAATGAGATTGGAAGTGTAGAGAAATTCCGGAATTATTGA	:	720
	* 680 * 700 * 720		
LpCSa :	GGGAGTGAAGAACAGGAAGCGGAAATGTCGGTTGGCACCCTGTGTATAAGAATTA	:	780
	* 740 * 760 * 780		
LpCSa :	TGATCCTCGTGCTAAAGTCATCCGGAAAGTTAGCGGAGGAGGTTTCACGATTGTGGACG	:	840
	* 800 * 820 * 840		
LpCSa :	GGATCCTCTTATCGAGGTAGCTGTTGGAGAAGGCAGCACTGTCAGACGAGTATT	:	900
	* 860 * 880 * 900		
LpCSa :	TATCAAGAGGAAGCTGTATCCAAATGTGGATTTTATTCTGGCTAATATAGGGCAAT	:	960
	* 920 * 940 * 960		

\* 980 \* 1000 \* 1020  
LpCSa : GGGATTCCCTACAGAGTTTCCCTGTTCTGAGTCAGTCGCATGGCTGGTTGGTT : 1020

\* 1040 \* 1060 \* 1080  
LpCSa : AGCACATTGGAAGGAGTCACTTGATGACCCCGACAATAAAATTATGAGGCCAACAGGT : 1080

\* 1100 \* 1120 \* 1140  
LpCSa : ATACACCGGTACTGGCTAAGGCATTACACCCAGTGAGAGAACGGGTGCCATCAAGCGA : 1140

\* 1160 \* 1180 \* 1200  
LpCSa : CAGTGAGCAGCTGGGAGATCGCTACATCAAACGCGACGAGGCGTCGGCGTGGCT : 1200

\* 1220 \* 1240 \* 1260  
LpCSa : TGCCCTGTAGAACAGTCTGCATGATAACAGCATACTCCACACAATAAACAGCTGCCA : 1260

\* 1280 \* 1300 \* 1320  
LpCSa : AGGGCCACGGCTGCTTAAATCTGGAGCTGCTATACTGTGTTATCACGTATATATAGGC : 1320

\* 1340 \* 1360 \* 1380  
LpCSa : AATAAAACTAATAATGCCGCCAGGACACTCACTGGTGGTCATGTGAAGTTGGTAGAA : 1380

\* 1400 \* 1420 \* 1440  
LpCSa : TGCACTTGTAACGTGTTAATTGTTATCCTGCAATGTACGCTCTAAACTGTTCAAG : 1440

\* 1460 \* 1480 \* 1500  
LpCSa : TATCTTGAAAGTCTTAATCATGTGGACCAATGAAGACATAGATCAAGTTCTTGCATGGG : 1500

\* 1520 \* 1540 \*  
LpCSa : CGGCGGCTGTTCTTGGAAAAAACTTTATGGGAGTCCTTTTACCA : 1550

ure 2 Deded amino acid sequence of LpCSa

\* 20 \* 40 \* 60  
LpCSa : YIDGDEGILRYRGYPIEEVAESSSFVEVAYLLMYGNLPTQSQLAGWEFAISQHSAVPQGL : 60

\* 80 \* 100 \* 120  
LpCSa : LDIIQSMPHDAHPMGVLASAMSTLSVFHPDANPALRGQDLYKSKQVRDKQIVRVLGKAPV : 120

\* 140 \* 160 \* 180  
LpCSa : IAAAAYLRLLAGRPFVLPSPNNLSYSENFLYMLDSMGDKDYKPNPRLARVLDVLFILHAEHE : 180

\* 200 \* 220 \* 240  
LpCSa : MNCSTA AVRHLASSGV DVFTALSGAVGALYGPLHGGANEAVL KMLNEIGS VENIPEFIEG : 240

\* 260 \* 280 \* 300  
LpCSa : VKNRKRKMSGFGHRVYKNYDPRAKVIRKLAEEVFTIVGRDPLIEVALEKAALSDEYFI : 300

\* 320 \* 340 \* 360  
LpCSa : KRKLYPNVDFYSGLIYRAMGFPTEFFPVLFAVPRMAGWLAHWKESLDDPDNKIMRPQQVY : 360

\* 380 \* 400  
LpCSa : TGTWLRHYTPVRERVPSSDSEQLGQIATSNATRRRRAGSAL : 401

Figure 3 Nucleotide sequences of nucleic acid fragments contributing to the consensus contig sequence LpCSa

	*	20	*	40	*	60	
LpCSa1 :		GNNTTATATTGACGGGGATGAGGAATTCTTCGCTACAGAGGCTATC	GAATTGAGGGAGGT				: 60
LpCSa2 :		-----					: -
LpCSa3 :		-----					: -
LpCSa4 :		-----					: -
LpCSa5 :		-----					: -
LpCSa6 :		-----					: -
LpCSa7 :		-----					: -
LpCSa8 :		-----					: -
	*	80	*	100	*	120	
LpCSa1 :		GGCTGAAAGCAGCTCGTTGTTGAGGTGCCTACCTCTTAATGTATG	GAATTTGCCCCAC				: 120
LpCSa2 :		-----					: -
LpCSa3 :		-----					: -
LpCSa4 :		-----					: -
LpCSa5 :		-----					: -
LpCSa6 :		-----					: -
LpCSa7 :		-----					: -
LpCSa8 :		-----					: -
	*	140	*	160	*	180	
LpCSa1 :		CCAGAGTCAACTGGCAGGCTGGGAGTTGCAATTTCG	CAGCACTCTG	GTGTTCCCTCAAGG			: 180
LpCSa2 :		-----	GCAGGCTGGGAGTTGCAATTTCGCA	CACTCTG	GTGTTCCCTCAAGG	N	: 46
LpCSa3 :		-----					: -
LpCSa4 :		-----					: -
LpCSa5 :		-----					: -
LpCSa6 :		-----					: -
LpCSa7 :		-----					: -
LpCSa8 :		-----					: -
	*	200	*	220	*	240	
LpCSa1 :		ACTCTTGGATATAATACAATCAATGCC	CATGATGCC	ACCCATGGGTGTC	CTTGCCAG		: 240
LpCSa2 :		ACTCTTGGATATAATACAATCAATGCC	CATGATGCC	ACCCATGGGTGTC	CTTGCCAG		: 106
LpCSa3 :		-----					: -
LpCSa4 :		-----					: -
LpCSa5 :		-----					: -
LpCSa6 :		-----					: -
LpCSa7 :		-----					: -
LpCSa8 :		-----					: -
	*	260	*	280	*	300	
LpCSa1 :		TGCAATGAGCACACTTCAGTCTTCCATCCAGATGCAAAACCC	TGCTCT	TAGAGGTCAAGA			: 300
LpCSa2 :		TGCAATGAGCACACTTCAGTCTTCCATCCAGATGCAAAACCC	TGCTCT	TAGAGGTCAAGA			: 166
LpCSa3 :		-----					: -
LpCSa4 :		-----					: -
LpCSa5 :		-----					: -
LpCSa6 :		-----					: -
LpCSa7 :		-----					: -
LpCSa8 :		-----					: -

	*            320            *	340		*            360	
LpCSa1 :	TCTATACAAGTCGAAGCAGGTTAGGGATAAGCAAATTGTACGAGTTCTGGAAAGGCACC				: 360
LpCSa2 :	TCTATACAAGTCGAAGCAGGTTAGGGATAAGCAAATTGTACGAGTTCTGGAAAGGCACC				: 226
LpCSa3 :	-----				:
LpCSa4 :	-----				:
LpCSa5 :	-----				:
LpCSa6 :	-----				:
LpCSa7 :	-----				:
LpCSa8 :	-----				:
	*            380            *	400		*            420	
LpCSa1 :	AGTAATAGCAGCTGCAGCCTATCTGAGATTAGCAGGAAGGCC	TTTGT	CCTTC	CTTCAAA	: 420
LpCSa2 :	AGTAATAGCAGCTGCAGCCTATCTGAGATTAGCAGGAAGGCC	TTTGT	CCTTC	CTTCAAA	: 286
LpCSa3 :	-----				:
LpCSa4 :	-----				:
LpCSa5 :	-----				:
LpCSa6 :	-----				:
LpCSa7 :	-----				:
LpCSa8 :	-----				:
	*            440            *	460		*            480	
LpCSa1 :	TAATCTCTCTTATTCA	GAAA	ATTCTTG	TATGCTGGACTCTATGGGTGACAAAGATTA	: 480
LpCSa2 :	TAATCTCTCTTATTCA	GAAA	ATTCTTG	TATGCTGGACTCTATGGGTGACAAAGATTA	: 346
LpCSa3 :	-----				:
LpCSa4 :	-----				:
LpCSa5 :	-----				:
LpCSa6 :	-----				:
LpCSa7 :	-----				:
LpCSa8 :	-----				:
	*            500            *	520		*            540	
LpCSa1 :	TAAGCCAAATCCCAGACTTGCCC	GGGT	CTGGATGTC	CCTTTATTCTCATGCTGAACA	: 540
LpCSa2 :	TAAGCCAAATCCCAGACTTGCCC	GGGT	CTGGATGTC	CCTTTATTCTCATGCTGAACA	: 406
LpCSa3 :	-----			NTNTGCTG-ACA	: 12
LpCSa4 :	-----				:
LpCSa5 :	-----				:
LpCSa6 :	-----				:
LpCSa7 :	-----				:
LpCSa8 :	-----				:
	*            560            *	580		*            600	
LpCSa1 :	CGAAATGAACTGCTCAACAGCTGCTGTTAGGCACCTTGCTTCAAGTGGTGT	CGATGTCTT			: 600
LpCSa2 :	CGAAATGAACTGCTCAACAGCTGCTGTTAGGCACCTTGCTTCAAGTGGTGT	CGATGTCTT			: 466
LpCSa3 :	CGAAATGANCTGCTCAACAGCTGCTGTTAGGCACCTTGCTTCAAGTGGTGT	CGATGTCTT			: 72
LpCSa4 :	-----				:
LpCSa5 :	-----				:
LpCSa6 :	-----				:
LpCSa7 :	-----				:
LpCSa8 :	-----				:
	*            620            *	640		*            660	
LpCSa1 :	CACTGCTCTTCTGGT	GCTGTTGGAGCTCTATATGGTCC	ACTGCATGG	GGCGCAAATGA	: 660
LpCSa2 :	CACTGCTCTTCTGGT	GCTGTTGGAGCTCTATATGGTCC	ACTGCATGG	GGCGCAAATGA	: 526
LpCSa3 :	CACTGCTCTTCTGGT	GCTGTTGGAGCTCTATATGGTCC	ACTGCATGG	GGCGCAAATGA	: 132
LpCSa4 :	-----				:
LpCSa5 :	-----				:
LpCSa6 :	-----				:
LpCSa7 :	-----				:
LpCSa8 :	-----				:

	*	680	*	700	*	720	
LpCSa1 :	NGCGGTACTT	AAATGTTAATGAGATTGGAAAGTAGAGAATATTCCGGAAATTCAATTGA					: 719
LpCSa2 :	GGCGGTACTT	AAAATGTTAATGAGATTGGAAAGTAGAGAATATTCCGGAAATTCAATTGA					: 586
LpCSa3 :	GGCGGTACTT	AAAATGTTAATGAGATTGGAAAGTAGAGAATATTCCGGAAATTCAATTGA					: 192
LpCSa4 :	-	-		-			:
LpCSa5 :	-	-		-			:
LpCSa6 :	-	-		-			:
LpCSa7 :	-	-		-			:
LpCSa8 :	-	-		-			:
	*	740	*	760	*	780	
LpCSa1 :	GGGAGTGAAGAACAGGAAGCGGAAAATGTCTGG	NTTGGGCACN	-				: 763
LpCSa2 :	GGGAGTGAAGAACAGGAAGCGGAAAATGTCTGG	NTTGGGCACCGTGTGTATAAGAATT	A				: 646
LpCSa3 :	GGGAGTGAAGAACAGGAAGCGGAAAATGTCTGG	CTTGGGCACCGTGTGTATAAGAATT	A				: 252
LpCSa4 :	-	-	-	-	-	-	: 2
LpCSa5 :	-	-	-	-	-	-	:
LpCSa6 :	-	-	-	-	-	-	:
LpCSa7 :	-	-	-	-	-	-	:
LpCSa8 :	-	-	-	-	-	-	:
	*	800	*	820	*	840	
LpCSa1 :	-	-	-	-	-	-	:
LpCSa2 :	TGATCCTCGTCTAAAGTCATCCGGAAAGTTAGCGGN	-	-				: 682
LpCSa3 :	TGATCCTCGTCTAAAGTCATCCGGAAAGTTAGCGGAGGAGGTTTCAGGATTGTGGGACG	-					: 312
LpCSa4 :	T	ATCCTCGGCTAAAGTCAT	CCGGAGTTAGCGGAGGAGGTTTCAGGATTGTGGGACG	-			: 61
LpCSa5 :	-	-	GGAAGTTAGCGGAGGAGGTTTCAGGATTGTGGGACG	-			: 37
LpCSa6 :	-	-	-	-	-	-	:
LpCSa7 :	-	-	-	-	-	-	:
LpCSa8 :	-	-	-	-	-	-	:
	*	860	*	880	*	900	
LpCSa1 :	-	-	-	-	-	-	:
LpCSa2 :	-	-	-	-	-	-	:
LpCSa3 :	GGATCCTCTTATCGAGGTAGCTGTTGCTTGGAGAAGG	AGCACTGT	CAGACGAGTATTT				: 372
LpCSa4 :	GGATCCTCTTATCGAGGTAGCTGTTGCTTGGAGAAGG	CAGCACTGT	CAGACGAGTATTT				: 121
LpCSa5 :	GG	NTCCTCTTATCGAGGTAGCTGTTGCTTGGAGAAGG	CAGCACTGT	CAGACGAGTATTT			: 97
LpCSa6 :	-	-	TNN	CAGACGAGTATTT			: 16
LpCSa7 :	-	-	-	GTCAGACGAGTATTT			: 15
LpCSa8 :	-	-	-	-	-	-	:
	*	920	*	940	*	960	
LpCSa1 :	-	-	-	-	-	-	:
LpCSa2 :	-	-	-	-	-	-	:
LpCSa3 :	TATCAAGAGGAAGCTGTATCCAAATGTGGATTTTATTCTGGCTAA	TATATAGGGCAAT	-				: 432
LpCSa4 :	TATCAAGAGGAAGCTGTATCCAAATGTGGATTTTATTCTGGCTAA	TATATAGGGCAAT	-				: 181
LpCSa5 :	TATC	EAGAGGAAGCTGTATCCAAATGTGGATTTTATTCTGGCTAA	TATATAGGGCAAT	-			: 157
LpCSa6 :	TATCAAGAGGAAGCTGTATCCAAATGTGGATTTTATTCTGGCTAA	TATATAGGGCAAT	-				: 76
LpCSa7 :	TATCAAGAGGAAGCTGTATCCAAATGTGGATTTTATTCTGGCTAA	TATATAGGGCAAT	-				: 75
LpCSa8 :	-	-	-	-	-	-	:
	*	980	*	1000	*	1020	
LpCSa1 :	-	-	-	-	-	-	:
LpCSa2 :	-	-	-	-	-	-	:
LpCSa3 :	GGGATTCCCTACAGAGTTTCCCTGTTCTGTTGCAGTCCTCGCAT	GGCTGGTTGGTT	-				: 492
LpCSa4 :	GGGATTCCCT	CAGAGTTTCCCTGTTCTGTTGCAGTCCTCGCAT	GGCTGGTTGGTT	-			: 241
LpCSa5 :	GGGATTCCCTACAGAGTTTCCCTGTTCTGTTGCAGTCCTCGCAT	GGCTGGTTGGTT	-				: 217
LpCSa6 :	GGGATTCCCTACAGAGTTTCCCTGTTCTGTTGCAGTCCTCGCAT	GGCTGGTTGGTT	-				: 136
LpCSa7 :	GGGATTCCCTACAGAGTTTCCCTGTTCTGTTGCAGTCCTCGCAT	GGCTGGTTGGTT	-				: 135
LpCSa8 :	-	-	-	-	-	-	:

	*	1040	*	1060	*	1080	:	-
LpCSa1 :	-	-	-	-	-	-	:	-
LpCSa2 :	-	-	-	-	-	-	:	-
LpCSa3 :	AGCACATTGGAAGGAGTCACTTGATGACCCCGACAATAAAATTATGAGGCCAACAGGT						:	552
LpCSa4 :	AGCACATTGGAAGGAGTCACTTGATGACCCCGACAATAAAATTATGAGGCCAACAGGT						:	301
LpCSa5 :	AGCACATTGGAAGGAGTCACTTGATGACCCCGACAATAAAATTATGAGGCCAACAGGT						:	277
LpCSa6 :	AGCACATTGGAAGGAGTCACTTGATGACCCCGACAATAAAATTATGAGGCCAACAGGT						:	196
LpCSa7 :	AGCACATTGGAAGGAGTCACTTGATGACCCCGACAATAAAATTATGAGGCCAACAGGT						:	195
LpCSa8 :	-	-	-	-	-	-	:	-
	*	1100	*	1120	*	1140	:	-
LpCSa1 :	-	-	-	-	-	-	:	-
LpCSa2 :	-	-	-	-	-	-	:	-
LpCSa3 :	ATACACCGTACTTGGCTAAGGCATTACACCCCGACTGAGAGAACGGGTGCCATCAAGCGA						:	612
LpCSa4 :	ATACACCGTACTTGGCTAAGGCATTACACCCCGACTGAGAGAACGGGTGCCATCAAGCGA						:	361
LpCSa5 :	ATACACCGTACTTGGCTAAGGCATTACACCCCGACTGAGAGAACGGGTGCCATCAAGCGA						:	337
LpCSa6 :	ATACACCGTACTTGGCTAAGGCATTACACCCCGACTGAGAGAACGGGTGCCATCAAGCGA						:	256
LpCSa7 :	ATACACCGTACTTGGCTAAGGCATTACACCCCGACTGAGAGAACGGGTGCCATCAAGCGA						:	255
LpCSa8 :	-	-	-	-	-	-	:	-
	*	1160	*	1180	*	1200	:	-
LpCSa1 :	-	-	-	-	-	-	:	-
LpCSa2 :	-	-	-	-	-	-	:	-
LpCSa3 :	CAGTGAGCAGCTGGCAGATCGACTACATCAAACCGCAGGAGCGTCCGGCGTGGCTTC						:	672
LpCSa4 :	CAGTGAGCAGCTGGCAGATCGCTACATCAAACCGCAGGAGCGTCCGGCGTGGCTTC						:	421
LpCSa5 :	CAGTGAGCAGCTGGCAGATCGCTACATCAAACCGCAGGAGCGTCCGGCGTGGCTTC						:	397
LpCSa6 :	CAGTGAGCAGCTGGCAGATCGCTACATCAAACCGCAGGAGCGTCCGGCGTGGCTTC						:	316
LpCSa7 :	CAGTGAGCAGCTGGCAGATCGCTACATCAAACCGCAGGAGCGTCCGGCGTGGCTTC						:	315
LpCSa8 :	GGCAGATCGCTACATCAAACCGCAGGAGCGTCCGGCGTGGCTTC						:	45
	*	1220	*	1240	*	1260	:	-
LpCSa1 :	-	-	-	-	-	-	:	-
LpCSa2 :	-	-	-	-	-	-	:	-
LpCSa3 :	TGCCCTGTAGAACAGTCTGCATGATAACAGCATACTGACAGTCCACACAATAACCAAGCTGCCA						:	732
LpCSa4 :	TGCCCTGTAGAACAGTCTGCATGATAACAGCATACTGACAGTCCACACAATAACCAAGCTGCCA						:	481
LpCSa5 :	TGCCCTGTAGAACAGTCTGCATGATAACAGCATACTGACAGTCCACACAATAACCAAGCTGCCA						:	457
LpCSa6 :	TGCCCTGTAGAACAGTCTGCATGATAACAGCATACTGACAGTCCACACAATAACCAAGCTGCCA						:	376
LpCSa7 :	TGCCCTGTAGAACAGTCTGCATGATAACAGCATACTGACAGTCCACACAATAACCAAGCTGCCA						:	375
LpCSa8 :	TGCCCTGTAGAACAGTCTGCATGATAACAGCATACTGACAGTCCACACAATAACCAAGCTGCCA						:	105
	*	1280	*	1300	*	1320	:	-
LpCSa1 :	-	-	-	-	-	-	:	-
LpCSa2 :	-	-	-	-	-	-	:	-
LpCSa3 :	AGGCCACGGCTGCTTAAATN						:	753
LpCSa4 :	AGGCCACGGCTGCTTAAATCTGGGAGCTGCTATACTTGTGTTATCAGGTATATGAGC						:	541
LpCSa5 :	AGGCCACGGCTGCTTAAATCTGGGAGCTGCTATACTTGTGTTATCAGGTATATAGGC						:	517
LpCSa6 :	AGGCCACGGCTGCTTAAATCTGGGAGCTGCTATACTTGTGTTATCAGGTATATAGGC						:	436
LpCSa7 :	AGGCCACGGCTGCTTAAATCTGGGAGCTGCTATACTTGTGTTATCAGGTATATAGGC						:	435
LpCSa8 :	AGGCCACGGCTGCTTAAATCTGGGAGCTGCTATACTTGTGTTATCAGGTATATAGGC						:	165
	*	1340	*	1360	*	1380	:	-
LpCSa1 :	-	-	-	-	-	-	:	-
LpCSa2 :	-	-	-	-	-	-	:	-
LpCSa3 :	-	-	-	-	-	-	:	-
LpCSa4 :	AATAAACTAATAATGCCGCCAGGACACTTCACTGGTGGTCATGTGAATTGGTAGTAGAA						:	601
LpCSa5 :	AATAAACTAATAATGCCGCCAGGACACTTCACTGGTGGTCATGTGAATTGGTAGTAGAA						:	577
LpCSa6 :	AATAAACTAATAATGCCGCCAGGACACTTCACTGGTGGTCATGTGAATTGGTAGTAGAA						:	496
LpCSa7 :	AATAAACTAATAATGCCGCCAGGACACTTCACTGGTGGTCATGTGAATTGGTAGTAGAA						:	495
LpCSa8 :	AATAAACTAATAATGCCGCCAGGACACTTCACTGGTGGTCATGTGAATTGGTAGTAGAA						:	225

	*	1400	*	1420	*	1440
CsA1 :	-	-	-	-	-	:
LpCSa2 :	-	-	-	-	-	:
LpCSa3 :	-	-	-	-	-	:
LpCSa4 :	TGCACTTGTAAACGTGTTAATTGTTATCCTGCAATGTACGCTCTATAAACTGTTCA					: 661
LpCSa5 :	TGCACTTGTAAACGTGTTAATTGTTATCCTGCAATGTACGCTCTATAAACTGTTCA					: 637
LpCSa6 :	TGCACTTGTAAACGTGTTAATTGTTATCCTGCAATGTACGCTCTATAAACTGTTCA					: 556
LpCSa7 :	TGCACTTGTAAACGTGTTAATTGTTATCCTGCAATGTACGCTCTATAAACTGTTCA					: 555
LpCSa8 :	TGCACTTGTAAACGTGTTAATTGTTATCCTGCAATGTACGCTCTATAAACTGTTCA					: 285

	*	1460	*	1480	*	1500	:
LpCSa1 :	-	-	-	-	-	-	-
LpCSa2 :	-	-	-	-	-	-	-
LpCSa3 :	-	-	-	-	-	-	-
LpCSa4 :	TG	TCTTGAAAGTCTTAATCATGTGGACCAA	-	GAAGACATAGATCAAG	T	TCTTGACATGGG	: 720
LpCSa5 :	TAT	TCTTGAAAGTCTTANTC	CNNNNAAAAA	-	-	-	: 666
LpCSa6 :	TAT	TCTTGAAAGTCTTAATCATGTGGACCAA	-	GAAGACATAGATCAAG	T	TCTTGACATGGG	: 615
LpCSa7 :	TAT	TCTTGAAAGTCTTAATCATGTGGACCAA	ATC	AAAAAAA	AAAAAAA	-	: 597
LpCSa8 :	TAT	TCTTGAAAGTCTTAA	AAAAAAA	-	-	-	: 310

	*	1520	*	1540	*
LpCSa1 :	- - - - -				:
LpCSa2 :	- - - - -				:
LpCSa3 :	- - - - -				:
LpCSa4 :	CGGCGGCTGTTCTTGNNAAAAAA	- - - - -			: 745
LpCSa5 :	- - - - -				:
LpCSa6 :	CGGCGGCTGTTCTTGCTGTTCCCT	CTTTTTATGGGAGTCTTTTTAACC			: 665
LpCSa7 :	- - - - -				:
LpCSa8 :	- - - - -				:

Figure 4 Consensus contig nucleotide sequence of LpCSb

LpCSb :	CTTCTCCCTGTNACTGCTCTCCAATGACACAGTTACCACTGGAGTGATGGCACTCCAAG	:	60
	* 20 * 40 * 60		
LpCSb :	TTGAGAGTGAATTGCAAAGGCTTATGAGAAGGAAATCATAAATCAAAGTTCTGGGAGC	:	120
	* 80 * 100 * 120		
LpCSb :	CTACATATGAAGATAGCTAAATTGATTGCTCGGCTTCCACAAGTGGCTTCATATGTTT	:	180
	* 140 * 160 * 180		
LpCSb :	ACCCGAGAATTTCAGGACGGAAAATATTGCAGCTGATAATACTGGACTACGCAG	:	240
	* 200 * 220 * 240		
LpCSb :	CTAATTTTCACACATGCTGGTTTGATGACCCCCAAATGCTGGAGTTGATGCGCCTAT	:	300
	* 260 * 280 * 300		
LpCSb :	ACATAACAATTACACTGATCACGAAGGAGGGAAATGTTAGTGCTCATGCTGGGCATCTGG	:	360
	* 320 * 340 * 360		
LpCSb :	TTGGAAGTGCTCTGTCAGATCCTTATCTTCTTGCAGCGGCAGTGAACGGTTAGCTG	:	420
	* 380 * 400 * 420		
LpCSb :	GACCACTGCACGGCTGGCTAACATTACAACGTGATCAGCTAAAGAATATGTTGAAAGACACTGAAGA	:	480
	* 440 * 460 * 480		
LpCSb :	AAACCGGGAGTAACATTACAACGTGATCAGCTAAAGAATATGTTGAAAGACACTGAAGA	:	540
	* 500 * 520 * 540		
LpCSb :	GTGGAAAGGTTGTTCTGGCTATGGTCATGGAGTTCTACGTAATACAGATCCACGATACT	:	600
	* 560 * 580 * 600		
LpCSb :	CGTGCCAAAGGGAGTTGCAGTGAAGTATTACCGAAGACCCACTTTCCAAGTGGCT	:	660
	* 620 * 640 * 660		
LpCSb :	CCAAGTTGTACGAAGTTGTGCCTCCTATCCTCACCGAGTTAGGCAAGGTAAAAAACCCAT	:	720
	* 680 * 700 * 720		
LpCSb :	GGCCTAATGTTGATGTCACAGTGGAGTTTGCTCAACCACCTCGGATTAGTTGAAGCAC	:	780
	* 740 * 760 * 780		
LpCSb :	GGTACTACACTGTCTTGGCTCGGCCTCAAGGAGCATGGGAATTGGATCTCAGCTCATT	:	840
	* 800 * 820 * 840		
LpCSb :	GGGACCGTGCCTCGGCCTGCCACTTGAAAGACCGAAGAGTGTCAACCACGGAGTGGCTGG	:	900
	* 860 * 880 * 900		
LpCSb :	AAAACCACTGCAAGAAGGCTGCAGCTGAAGCTACACCAATGCTCGTTACAAATCAG	:	960
	* 920 * 940 * 960		

\* 980 \* 1000 \* 1020

LpCSb : GCCGTCTTGATGTTAATAATGACTGAGCATAAGTAGGCATGGTTAGCCTGTTTAC : 1020

\* 1040 \* 1060 \* 1080

LpCSb : ATCTTCGTTTCTGGCCAATAACTGGAGCAAGAGGGTCACAGACGGTAGAATTGTAA : 1080

\* 1100 \* 1120 \* 1140

LpCSb : CCACCGNTACTTGAACACCGAACATCANTAAATGTCATTGGCATAAAGAGATTAGGACAT : 1140

\* 1160

LpCSb : GACACATAAGTTTATGTGTCGCTCG : 1167

Figure 5 Dededuced amino acid sequence of LpCSb

\* 20 \* 40 \* 60  
LpCSb : SPCXCSPMTQFTTGVMALQVESEFAKAYEKGIHKSKFWEPTYEDSLNLIARLPQVASYVY : 60

\* 80 \* 100 \* 120  
LpCSb : RRIFKDGTIAADNTLDYAANFSHMLGFDDPKMLEMRLYITIHTDHEGGNVSAHAGHLV : 120

\* 140 \* 160 \* 180  
LpCSb : GSALSDPYLSFAAALNGLAGPLHGLANQEVLXWIKSVMEEETGSNITTDQLKEYVWKTLKS : 180

\* 200 \* 220 \* 240  
LpCSb : GKVVPGYGHGVLRNTDPRYSCQREFALKYLPEDPLFQLVSKLYEVVPPILTELGKVKNPW : 240

\* 260 \* 280 \* 300  
LpCSb : PNVDAAHSGVLLNHFGLVEARYYTVLFGVSRSMGIGSQLIWDRALGLPLERPKSVTMEWLE : 300

LpCSb : NHCKKAAA : 308

Figure 6 Nucleotide sequences of nucleic acid fragments contributing to the consensus contig sequence LpCSb

	*            20            *	*            40            *	*            60	
LpCSb1 :	CTTCTCCCTGTNACTGCTCTCCAATGACACAGTTACCACTGGAGTGATGGCACTCCAAG			: 60
LpCSb2 :	-			:
LpCSb3 :	-			:
LpCSb4 :	-			:
	*            80            *	*            100            *	*            120	
LpCSb1 :	TTGAGAGTGAATTGCAAAGGCTTATGAGAAGGAAATTCAAAGTTCTGGGAGC			: 120
LpCSb2 :	-			:
LpCSb3 :	-			:
LpCSb4 :	-			:
	*            140            *	*            160            *	*            180	
LpCSb1 :	CTACATATGAAGATAAGCTTAAATTGATTGCTCGGCTTCCACAAGTGGCTTCATAATGTTT			: 180
LpCSb2 :	-			:
LpCSb3 :	-			:
LpCSb4 :	-			:
	*            200            *	*            220            *	*            240	
LpCSb1 :	ACCGGAGAATTTCAAGGACGGAAAACATTGCAGCTGATAATACTGGACTACGCAG			: 240
LpCSb2 :	-			:
LpCSb3 :	-			:
LpCSb4 :	-			:
	*            260            *	*            280            *	*            300	
LpCSb1 :	CTAATTTTACACATGCTGGTTTGATGACCCAAAATGCTGGAGTGATGCGCTAT			: 300
LpCSb2 :	-			:
LpCSb3 :	-			:
LpCSb4 :	-			:
	*            320            *	*            340            *	*            360	
LpCSb1 :	ACATAACAATTCACACTGATCACGAAGGAGGAATGTTAGTGCTCATGCTGGGCATCTGG			: 360
LpCSb2 :	-			:
LpCSb3 :	-			:
LpCSb4 :	-			:
	*            380            *	*            400            *	*            420	
LpCSb1 :	TTGGAAGTGCTCTGTCAGATCCTTATCTTCTTTGCAGCGGCACTGAACGGTTAGCTG			: 420
LpCSb2 :	-			:
LpCSb3 :	-			:
LpCSb4 :	-			:
	*            440            *	*            460            *	*            480	
LpCSb1 :	GACCAC TGACGGCTTGGCTAACAGGAAGTGTGTATGGATCAAATCTGTGATGGAAG			: 480
LpCSb2 :	-			:
LpCSb3 :	-			:
LpCSb4 :	-			:
	*            500            *	*            520            *	*            540	
LpCSb1 :	AAACCGGGAGTAACATTACAAC TGATCAGCTAACAGAATATGTTGGAAGACACTGAAGA			: 540
LpCSb2 :	-			:
LpCSb3 :	-			:
LpCSb4 :	-			:

	*            560            *	*            580            *	*            600	
LpCSb1 :	GTGGAAAGGTTGTCCTGGCATGGAGTTCTACGTAATACAGATCCACGATACT			: 600
LpCSb2 :	GTGGAAAGGTTGTCCTGGCATGGAGTTCTACGTAATACAGATCCACGATACT			: 143
LpCSb3 :	GTGGAAAGGTTGTCCTGGCATGGAGTTCTACGTAATACAGATCCACGATACT			: 67
LpCSb4 :	-----			:
	*            620            *	*            640            *	*            660	
LpCSb1 :	CGTGCCAAAGGGAGTTGCACTGAAGTATTTACCGAAGACCCACTTTCCAAC			: 660
LpCSb2 :	CGTGCCAAAGGGAGTTGCACTGAAGTATTTACCGAAGACCCACTTTCCAAC			: 203
LpCSb3 :	CGTGCCAAAGGGAGTNGNACTGAAGTATTTACCGAAGACCCACTTTCCAAC			: 127
LpCSb4 :	-----			:
	*            680            *	*            700            *	*            720	
LpCSb1 :	CCAAGTTGTA[TGAAGTTGTCCTCCTATCCTCAC]GAGTTAGGCAAGGTAAAAAACCCAT			: 720
LpCSb2 :	CCAAGTTGTA[CGAAGTTGTCCTCCTATCCTCACCGAG]TTAGGCAAGGTAAAAAACCCAT			: 263
LpCSb3 :	CCAAGTTGTA[CGAAGTTGTCCTCCTATCCTCACCGAG]TTAGGCAAGGTAAAAAACCCAT			: 187
LpCSb4 :	-----			:
	*            740            *	*            760            *	*            780	
LpCSb1 :	GGCCTAATGTTGATGCTCACAGNGGAGTTTGCTCAACCACCTCGGATTAGTTGAA-CAC			: 779
LpCSb2 :	GGCCTAATGTTGATGCTCACAGTGGAGTTTGCTCAACCACCTCGGATTAGTTGAAAGCAC			: 323
LpCSb3 :	GGCCTAATGTTGATGCTCACAGTGGAGTTTGCTCAACCACCTCGGATTAGTTGAAAGCAC			: 247
LpCSb4 :	-----			:
	*            800            *	*            820            *	*            840	
LpCSb1 :	GGNACTACACTGNCTTGNTCCGN-----			: 802
LpCSb2 :	GGTACTACACTGTCTTGTCGGCGTCTCAAGGAGCATGGGAATTGGATCTCAGCCATT			: 383
LpCSb3 :	GGTACTACACTGTCTTGTCGGCGTCTCAAGGAGCATGGGAATTGGATCTCAGCTCATTT			: 307
LpCSb4 :	-----GTTTGTGGATCCAGCTCATTT			: 22
	*            860            *	*            880            *	*            900	
LpCSb1 :	-----			:
LpCSb2 :	GGGACCGTGCCCTCGGCCTGCCACTTGAAAGACCGAAGAGTGTACCATGGAGTGGCTGG			: 443
LpCSb3 :	GGGACCGTGCCCTCGGCCTGCCACTTGAAAGACCGAAGAGTGTACCATGGAGTGGCTGG			: 367
LpCSb4 :	GGGTCGGTGCCCTCGGCCTGCCACTTGAAAGACCGAAGAGTGTACCATGGAGTGGCTGG			: 82
	*            920            *	*            940            *	*            960	
LpCSb1 :	-----			:
LpCSb2 :	AAAACCACTGCAAGAAGGCTGGCGCTGAAGCTACACCAATGCTTCGTTTACAAATCAG			: 503
LpCSb3 :	AAAACCACTGCAAGAAGGCTGGCGCTGAAGCTACACCAATGCTTGTGTTACAAATCAN			: 427
LpCSb4 :	AAAACCACTGCAAGAAGGCTGGCGCTGAAGCTACACCAATGCTTCGTTTACAAATCAG			: 142
	*            980            *	*            1000            *	*            1020	
LpCSb1 :	-----			:
LpCSb2 :	GCCGTCTTGATGTTAATAATGACTGAGCATAAGTTAGGCATGGTAGCCTGTTTACCC			: 563
LpCSb3 :	GCCGTCTTGATGTTAATAATGACTGAGCATAAGTTAGGCATGGTAGCCTGTTTACCC			: 487
LpCSb4 :	GCCGTCTTGATGTTAATAATGACTGAGCATAAGTTAGGCATGGTAGCCTGTTTACCC			: 202
	*            1040            *	*            1060            *	*            1080	
LpCSb1 :	-----			:
LpCSb2 :	ATCTTCGTTTCTGGCCAATAACTGGAGCAAGAGGCTACAGACGGTAGAATTGTAA			: 623
LpCSb3 :	ATNTTCGTTTCTGGCCAATAACTGGAGCAAGAGGCTACAGACGGTAGAATTGTAA			: 547
LpCSb4 :	ATCTTCGTTTCTGGCCAATAACTGGAGCAAGAGGCTACAGACGGTAGAATTGTAA			: 262

\* 1100 \* 1120 \* 1140

LpCSb1 :				:	-		
LpCSb2 :	CCACCGNTACTTGAACACCGAATCANTAAATGTCATTGGCATAAAGAGATTAGGACAT			:	683		
LpCSb3 :	CCACCGGTACTTGACACCGAATNANNAAATG	C	N	A	TTGGCATAAAGAGATTAGGACAT	:	606
LpCSb4 :	CCACCGTTACTTGAACACCGAATCA	G	T	A	TTGGCATAAAGAGATTAGGACAT	:	322

\* 1160

LpCSb1 :				:	-	
LpCSb2 :	GACACATAAGTTTATGTGNCGN	T	C	GG	:	710
LpCSb3 :	GACACATAAGTTTATGTGTCGCT	C	G	GG	:	633
LpCSb4 :	GACACATAAGTTTATGTGTCGCT	C	G	GA	:	349

Figure 7 Nucleotide sequence of LpCSc

\* 20 \* 40 \* 60  
LpCSc : TCNCCGTGGCCANAATNCCCCANCATTCAAATACCGCCCGTCAGCCACCAATCCTCCTAC : 60

\* 80 \* 100 \* 120  
LpCSc : CTTCTTATTCACCCCAACCGCCCAACATGTGTCTCCCACCGAANAAACACCTGCTAC : 120

\* 140 \* 160 \* 180  
LpCSc : CAACGGCCATAGCAACGGCACCAACGGGCCAATGGCTCCAAGGAAGGCTTCACAGGCGT : 180

\* 200 \* 220 \* 240  
LpCSc : CACGACCAGACAGAACCCCTCACCCCTACACACAAGAGGCCATATGCACCTGTTGGCGACTT : 240

\* 260 \* 280 \* 300  
LpCSc : TTTGTCAAATGTCGGCCGCTTCAGATTATCGAGAGCACATTAAGAGAGGGCGAGCAATT : 300

\* 320 \* 340 \* 360  
LpCSc : CGCCAACGCCACTTCGACCTTGAGGCTAAATCAAGATGCCAGAGCTCTGACAACTT : 360

\* 380 \* 400 \* 420  
LpCSc : TGGTGTTGACTACATTGAAGTTACCAGCCCTGCTGCCTCTGAGCAGTCAAGAAGGGACTG : 420

\* 440 \* 460 \* 480  
LpCSc : CGAAGCCCTTGCAAGCTCGGATTGAAAGCCAAGATCCTTACCCACGTACGATGCCACAT : 480

\* 500 \* 520 \* 540  
LpCSc : GGACGATGCCAGAACCGCTGTCGAGACTGGTGTGACGGCCTCGATGTCGTATTGGAAC : 540

\* 560 \* 580 \* 600  
LpCSc : CTCTGCGTACCTCCCGAGCACAGCCATGGCAAGGACATGACATACTACAAAAACACAGC : 600

\* 620 \*  
LpCSc : GCTGGAGGTGATTGAGTTGTCAAGAGCAAGGGAN : 635

ure 8 Deduced amino acid sequence of LpCSC

\* 20 \* 40 \* 60  
LpCSc : XRGXNXPXFKYRPSATNPPTFLFPPQPPNMCPPTEXTPATNGHSNGTNGANGSKEGFTGV : 60

\* 80 \* 100 \* 120  
LpCSc : TTRQNPHPTHKSPYAPVGDFLSNVGRFKIIESTLREGEQFANAYFDLEAKIKIARALDNF : 120

\* 140 \* 160 \* 180  
LpCSc : GVDYIEVTSPAASEQSRRDCEALCKLGLKAKILTHVRCHMDDARIAVETGVDGLDVVIGT : 180

\* 200 \*  
LpCSc : SAYLREHSHGKDMTYIKNTALEVIEFVKSKG : 211

Figure 9 Nucleotide sequence of LpCsd

\* 20 \* 40 \* 60  
LpCsd : GTGNTATGGNCANCCAGNANTCCTNCGTNCTGGCTNCCANANNAGNAANAAGCTATCGG : 60

\* 80 \* 100 \* 120  
LpCsd : CAACGACCTCAGCGATCAGGCCATCAAGGACTACCTGTGGTCCACCCTCAAGGCTGGCCA : 120

\* 140 \* 160 \* 180  
LpCsd : AGTCGTTCCCGGTTACGGACACGCCGTTCTCCGCAAGACCGACCCCCGCTACGTCTCCCA : 180

\* 200 \* 220 \* 240  
LpCsd : GCGCGAGTTCGCCCAGAACGCACCTTCCCGACGACCCAATGTTCAAGCTCGTCAGTCAGGT : 240

\* 260 \* 280 \* 300  
LpCsd : CTACAAGATCGCCCCGGTGTCTCACCGAGCACGGCAAGACCAAGAACCCCTACCCCAA : 300

\* 320 \* 340 \* 360  
LpCsd : CGTCGACGCCACTCCGGTGTCCCTCCAGTACTACGGCCTCACTGAGCAGAACTACTA : 360

\* 380 \* 400 \* 420  
LpCsd : CACCGTTCTTCGGTGTATCCCGTGCGCTCGGTGTCCCTCCCCAGCTTATCATTGACCG : 420

\* 440 \* 460 \* 480  
LpCsd : TGCCGTCGGTGCCCCCATTGAGAGGCCAAGTCTTCAGCACTGAGGCTTACGCCAAGTT : 480

\* 500 \* 520 \* 540  
LpCsd : GGTTGGTGCTAAGTTGTAAGCGCGTTACTGCAACGTGCTCTACAGCCAGGAGAATGTGGA : 540

\* 560 \* 580 \* 600  
LpCsd : GGAATTGTTAACATTCAAGAGATAACCTTGTCTGTAGAATTGCAATGTAAGGATAGG : 600

\* 620 \*  
LpCsd : GAATGGGAGCGTTACGGCGTACATCACTACATTN : 636

Figure 10 Deduced amino acid sequence of LpCsd

\* 20 \* 40 \* 60  
LpCsd : XYGXXXXPXXWPXXXXAIGNDLSDQAIKDYLWSTLKAGQVVPGYGHAVLRKTDPRYVSQ : 60

\* 80 \* 100 \* 120  
LpCsd : REFAQKHLPPDDPMFKLVSQVYKIAPGVLTEHGKTKNPYPNVDAHSGVLLQYYGLTEQNYY : 120

\* 140 \* 160  
LpCsd : TVLFGVSRALGVLPQLIIDRAVGAPIERPFSFSTEAYAKLVGAKL : 165

ure 11 Consensus contig nucleotide sequence of LpMDHa

\* 20 \* 40 \* 60  
LpMDHa : GGTTGGTTGCTGGTATCACCAATTCTGCCCTGTTCTCACAGGCAACTCCTTCGACTAATGC : 60

\* 80 \* 100 \* 120  
LpMDHa : ATTGTCTAGTGAAGACATCAAGGCTCTACCAAGAGGACACAGGAGGGTGGACAGAAAGT : 120

\* 140 \* 160 \* 180  
LpMDHa : TGTTGAGGCAAAGGCTGGAAAGGGATCTGCAACCTTGTCCATGGCGTATGCTGGCGCAGT : 180

\* 200 \* 220 \* 240  
LpMDHa : TTTTGGTGATGCATGCTTGAAGGGTCTGAACGGAGTTCCCTGACATTGTTGAATGCTCCTA : 240

\* 260 \* 280 \* 300  
LpMDHa : CGTGCAATCAACTATCACAGAACTGCCATTCTTCCTCCAAGGTGAGGCTCGGGAAGAA : 300

\* 320 \* 340 \* 360  
LpMDHa : TGGAGTCGAGGAAGTGCTTGGTTGGGTGAGCTGTCGGCCTTGAGAAGGAAGGTTGGA : 360

\* 380 \* 400 \* 420  
LpMDHa : AAGTCTCAAGGGTGAGCTCAAGTCTTCAATTGACAAGGGCATCGCGTTGCCAATGCGAG : 420

\* 440 \* 460 \* 480  
LpMDHa : TTAATTAATTTCAGATTATAGCAAACCAGGTCTAGTTAAGGGTCTGTTTGACTTT : 480

\* 500 \* 520 \* 540  
LpMDHa : TTGTTCAAGTGCTTTCTGCCCATCACGTGGCATGGAAGATTGAGCTTCACAATAAAA : 540

\* 560 \* 580 \* 600  
LpMDHa : ATCCGGCGGCGTAATGCCACAGAACATTACTTGACAAAGAGGAACTAGTTCGTGTCAAG : 600

\* 620 \* 640 \* 660  
LpMDHa : TTTTGAACTGGTACATTAACGAACAATTGCTGATGCACTTGAGAAAAAAAAATTGGGG : 660

\* 680 \*  
LpMDHa : GTGANTCCATTGGCCTCAAGCCAAAAAA : 696

ure 12 Dduced amino acid sequence of LpMDHa

\* 20 \* 40 \* 60  
LpMDHa : VGCWYHHSALFSQATPSTNALSSEDIKALTQEGGTEVVEAKAGKGSATLSMAYAGAV : 60

\* 80 \* 100 \* 120  
LpMDHa : FGDACLKGNGVPDIVECSYVQSTITELPFFASKVRLGKNGVEEVLGLGELSAFEKEGLE : 120

\* 140  
LpMDHa : SLKGELKSSIDKGIAFANAS : 140

Figure 13 Nucleotide sequences of nucleic acid fragments contributing to the consensus contig sequence LpMDHa

	*	20	*	40	*	60	
LpMDHa1 :		GTTGGTGTGCTGGTATCACCAATTCTGCCCTGTTCTCACAGGCAACTCCTTCGACTAATGC					: 60
LpMDHa2 :	-	GTTGGTGTGCTGGTATCACCAATTCTGCCCTGTTCTCACAGGCAACTCCTTCGACTAATGC					: 59
LpMDHa3 :	-	GTEGGTGTGCTGGTATCACCAATTCTGCCCTGTTCTCACAGGCAACTCCTTCGACTAATGC					: 59
LpMDHa4 :	-	-GGTTGGTGTGCTGGTATCACCAATTCTGCCCTGTTCTCACAGGCAACTCCTTCGACTAATGC					: 56
LpMDHa5 :	-						:
LpMDHa6 :	-						:
LpMDHa7 :	-						:
	*	80	*	100	*	120	
LpMDHa1 :		ATTGTCTAGTGAAGACATCAAGGCTCTACCAAGAGGACACAGGAGGGTGGGACAGAAAGT					: 120
LpMDHa2 :		ATTGTCTAGTGAAGACATCAAGGCTCTACCAAGAGGACACAGGAGGGTGGGACAGAAAGT					: 119
LpMDHa3 :		ATTGTCTAGTGAAGACATCAAGGCTCTACCAAGAGGACACAGGAGGGTGGGACAGAAAGT					: 119
LpMDHa4 :		ATTGTCTAGTGAAGACATCAAGGCTCTACCAAGAGGACACAGGAGGGTGGGACAGAAAGT					: 116
LpMDHa5 :	-	-					: 17
LpMDHa6 :	-						:
LpMDHa7 :	-						:
	*	140	*	160	*	180	
LpMDHa1 :		TGTTGAGGCAAAGGCTGGAAAGGGATCTGCAACCTTGTCCATGGCGTATGCTGGCGCAGT					: 180
LpMDHa2 :		TGTTGAGGCAAAGGCTGGAAAGGGATCTGCAACCTTGTCCATGGCGTATGCTGGCGCAGT					: 179
LpMDHa3 :		TGTTGAGGCAAAGGCTGGAAAGGGATCTGCAACCTTGTCCATGGCGTATGCTGGCGCAGT					: 179
LpMDHa4 :		TGTTGAGGCAAAGGCTGGAAAGGGATCTGCAACCTTGTCCATGGCGTATGCTGGCGCAGT					: 176
LpMDHa5 :		TGTTGAGGCAAAGGCTGGAAAGGGATCTGCAACCTTGTCCATGGCGTATGCTGGCGCAGT					: 77
LpMDHa6 :	-	-					:
LpMDHa7 :	-	-					:
	*	200	*	220	*	240	
LpMDHa1 :		TTTGTTGGTATGCATGCTGAAGGGTCTGAACGGAGTTCCCTGACATTGTTGAATGCTCCTA					: 240
LpMDHa2 :		TTTGTTGGTATGCATGCTGAAGGGTCTGAACGGAGTTCCCTGACATTGTTGAATGCTCCTA					: 239
LpMDHa3 :		TTTGTTGGTATGCATGCTGAAGGGTCTGAACGGAGTTCCCTGACATTGTTGAATGCTCCTA					: 239
LpMDHa4 :		TTTGTTGGTATGCATGCTGAAGGGTCTGAACGGAGTTCCCTGACATTGTTGAATGCTCCTA					: 236
LpMDHa5 :		TTTGTTGGTATGCATGCTGAAGGGTCTGAACGGAGTTCCCTGACATTGTTGAATGCTCCTA					: 137
LpMDHa6 :	-	-					:
LpMDHa7 :	-	-					:
	*	260	*	280	*	300	
LpMDHa1 :		CGTGAATCAACTATCACAGAACTGCCATTCTTGCCTCCAAGGTGAGGCTCGGGAAAGAA					: 300
LpMDHa2 :		CGTGAATCAACTATCACAGAACTGCCATTCTTGCCTCCAAGGTGAGGCTCGGGAAAGAA					: 299
LpMDHa3 :		CGTGAATCAACTATCACAGAACTGCCATTCTTGCCTCCAAGGTGAGGCTCGGGAAAGAA					: 299
LpMDHa4 :		CGTGAATCAACTATCACAGAACTGCCATTCTTGCCTCCAAGGTGAGGCTCGGGAAAGAA					: 296
LpMDHa5 :		CGTGAATCAACTATCACAGAACTGCCATTCTTGCCTCCAAGGTGAGGCTCGGGAAAGAA					: 197
LpMDHa6 :	-	-					: 17
LpMDHa7 :	-	-					: 2
	*	320	*	340	*	360	
LpMDHa1 :		TGGAGTCGAGGAAGTGCTGGTTGGGTGAGCTGTCGGCCTTGTGAGAAGGAAGGTTGGA					: 360
LpMDHa2 :		TGGAGTCGAGGAAGTGCTGGTTGGGTGAGCTGTCGGCCTTGTGAGAAGGAAGGTTGGA					: 359
LpMDHa3 :		TGGAGTCGAGGAAGTGCTGGTTGGGTGAGCTGTCGGCCTTGTGAGAAGGAAGGTTGGA					: 359
LpMDHa4 :		TGGAGTCGAGGAAGTGCTGGTTGGGTGAGCTGTCGGCCTTGTGAGAAGGAAGGTTGGA					: 356
LpMDHa5 :		TGGAGTCGAGGAAGTGCTGGTTGGGTGAGCTGTCGGCCTTGTGAGAAGGAAGGTTGGA					: 257
LpMDHa6 :		TGGAGTCGAGGAAGTGCTGGTTGGGTGAGCTGTCGGCCTTGTGAGAAGGAAGGTTGGA					: 77
LpMDHa7 :		TGGAGTCGAGGAAGTGCTGGTTGGGTGAGCTGTCGGCCTTGTGAGAAGGAAGGTTGGA					: 62

	* 380 * 400 * 420	
LpMDHa1 :	AAGTCTCAAGGGTGAGCTCAAGTCTTCAATTGACAAGGGCATCGCGTCGCCAATGCGAG	: 420
LpMDHa2 :	AAGTCTCAAGGGTGAGCTCAAGTCTTCAATTGACAAGGGCATCGCGTCGCCAATGCGAG	: 419
LpMDHa3 :	AAGTCTCAAGGGTGAGCTCAAGTCTTCAATTGACAAGGGCATCGCGTCGCCAATGCGAG	: 419
LpMDHa4 :	AAGTCTCAAGGGTGAGCTCAAGTCTTCAATTGACAAGGGCATCGCGTCGCCAATGCGAG	: 416
LpMDHa5 :	AAGTCTCAAGGGTGAGCTCAAGTCTTCAATTGACAAGGGCATCGCGTCGCCAATGCGAG	: 317
LpMDHa6 :	AAGTCTCAAGGGTGAGCTCAAGTCTTCAATTGACAAGGGCATCGCGTCGCCAATGCGAG	: 137
LpMDHa7 :	AAGTCTCAAGGGTGAGNTCAAGTCTTCAATTGACAAGGGCATCGCGTCGCCAATGCGAG	: 122
	* 440 * 460 * 480	
LpMDHa1 :	TTAATTAAATTTGCAGATTATAGCAAACCCAGGTCTAGTTAAGGGGCTCTG-----TTG-----TTT	: 475
LpMDHa2 :	TTAATTAAATTTGCAGATTATAGCAAACCCAGGTCTAGTTAAGGGGCTCTG-----TTG-----TTT	: 474
LpMDHa3 :	TTAATTAAATTTGCAGATTATAGCAAACCCAGGTCTAGTTAAGGGGCTCTG-----TTG-----TTT	: 474
LpMDHa4 :	TTAATTAAATTTGCAGATTATAGCAAACCCAGGTCTAGTTAAGGGGCTCTG-----TTG-----MTT	: 471
LpMDHa5 :	TTGATTAAATTTGCAGATTATAGCAAACCCAGGTCTAGTTGAGGGGCTGTGTTTGACTTT	: 377
LpMDHa6 :	TTGATTAAATTTGCAGATTATAGCAAACCCAGGTCTAGTTGAGGGGCTGTGTTTGACTTT	: 197
LpMDHa7 :	TTGATTAAATTTGCAGATTATAGCAAACCCAGGTCTAGTTGAGGGGCTGTGTTTGACTTT	: 182
	* 500 * 520 * 540	
LpMDHa1 :	TTGTTCAGTGCTTTCTGCCCATCACGTGGCATGGAAGATTGAGCTTCACAATAAAA	: 535
LpMDHa2 :	TTGTTCAGTGCTTTCTGCCCATCACGTGGCATGGAAGATTGAGCTTCACAATAAAA	: 534
LpMDHa3 :	TTGTTCAGTGCTTTCTGCCCATCACGTGGCATGNAAGATTGAGCTTCACAATAAAA	: 534
LpMDHa4 :	TTGNTCANNGCTTTCTGCCCATCACGTGGCATGNAAGATTGAGCTTCACAATAANNT	: 531
LpMDHa5 :	TTGTTCAGNGCTTTCTGCCCATCACGTGGCATGGAAGATTGAGCTTCACAATAAAA	: 437
LpMDHa6 :	TTGTTCAGTGCTTTCTGCCCATCACGTGGCATGGAAGATTGAGCTTCACAATAAAA	: 257
LpMDHa7 :	TTGTTCAGTGCTTTCTGCCCATCACGTGGCATGGAAGATTGAGCTTCACAATAAAA	: 242
	* 560 * 580 * 600	
LpMDHa1 :	ATCCGGCGCGTAATGCCACAGAACATTACTTGTACAAGAGGGAACTAGTCGTGTCAAG	: 595
LpMDHa2 :	ATCCGGCGCGTAATGCCACAGAACATTACTTGTACAAGAGGGAACTAGTCGTGTCAAG	: 594
LpMDHa3 :	ATCCGGCGCGTAATGCCACAGAACATTACTTGTACAAGAGGGAACTAGTCGTGTCAAG	: 594
LpMDHa4 :	ATNCNNGCGGN-----	: 544
LpMDHa5 :	ATCCGGCGCGTAATGCCACAGAACATTACTTGTACAAGAGGGAACTAGTCGGTNAAG	: 497
LpMDHa6 :	ATCCGGCGCGTAATGCCACAGAACATTACTTGTACAAGAGGGAACTAGTCGTGTCAAG	: 317
LpMDHa7 :	ATCCGGCGCGTAATGCCACAGAACATTACTTGTACAAGAGGGAACTAGTCGTGTCAAG	: 302
	* 620 * 640 * 660	
LpMDHa1 :	TTTTGAACTGGTACATTAACGAACAATTGCTGATGCACTTTGAGAAAAA-----	: 650
LpMDHa2 :	TTTTGAACTGGTACATTAACGAACAATTGCTGATGCACTTTGAGAAAAA-----	: 649
LpMDHa3 :	TTTTGAACTGGTACATTAACGAACAATTGCTGATGCACTTTGAGAAAAA-----	: 649
LpMDHa4 :	-----	: -
LpMDHa5 :	TTTTGAACTGGNACATTAACGAACAATTGCTGATGCACTTTGAGAAAAA-----	: 557
LpMDHa6 :	TTTTGAACTGGTACATTAACGAACAATTGCTGATGCACTTTGAGAACCGTCCTTTGGEG	: 377
LpMDHa7 :	TTTTGAACTGGTACATTAACGAACAATTGCTGAGAAAAA-----	: 345
	* 680 *	
LpMDHa1 :	-----	: -
LpMDHa2 :	-----	: -
LpMDHa3 :	-----	: -
LpMDHa4 :	-----	: -
LpMDHa5 :	G TGANTCCATTGGNCTNAAGCCAAAAA-----	: 589
LpMDHa6 :	T TGAATCCATTGCTTCAGTTAACGAANAAANAAA	: 413
LpMDHa7 :	-----	: -

ure 14 Consensus contig nucleotide sequence of LpMDHb

\* 20 \* 40 \* 60  
LpMDHb : TTTGGTNCTTTGCCGAGCGAGAAAGCTGTTGGTGTCAACCACCCCTGNGTTGTCGTGC : 60

\* 80 \* 100 \* 120  
LpMDHb : TAAAACCTTCTACGCTGGGAAGGCACACGTGCCAGTCACTGGGTGAATGTTCTGTTGT : 120

\* 140 \* 160 \* 180  
LpMDHb : TGGTGCCATGCTGGTGTACTATCCTGCCACAGTCTCACAGGCTACTCCTGCAAGTAA : 180

\* 200 \* 220 \* 240  
LpMDHb : TGCATTGTCCCAGGACCTTAAGGCCCTCACCAAGAGGACACAAGATGGTGGGACGGA : 240

\* 260 \* 280 \* 300  
LpMDHb : AGTTGTTGAAGCAAAGGCTGGAAAGGGCTCAGAACATTGTCATGGCATATGCTGGTGC : 300

\* 320 \* 340 \* 360  
LpMDHb : AGTATTTGGAGATGCATGCTGAAGGGCTCAATGGAGTTCCCTGACATTGTAGAGTGCTC : 360

\* 380 \* 400 \* 420  
LpMDHb : CTTTGTGCAATCAACCGTAACAGAGCTGCCATTCTTGCCTCCAAGGTAAGGCTCGGCAA : 420

\* 440 \* 460 \* 480  
LpMDHb : GAACGGAGTGGAGGAAGTGATTGGCTGGCGAGCTGTCCTGCCTCGAGAAGGAGGGTCT : 480

\* 500 \* 520 \* 540  
LpMDHb : GGAGAGCCTCAAGGGCGAGCTGNTGNCCATCGAGAAGGGTATCAAGTTCGCGCAGGA : 540

\* 560 \* 580 \* 600  
LpMDHb : GAGCTAGTCAACCTGCTCAGATTCTAACACTCCGCACATGAACTCGGTGGGATCTGATGA : 600

\* 620 \* 640 \* 660  
LpMDHb : ATTTTTGGTACGACTCCTTCACTGCCCTTCTCCTGGGGACATTGAGGCGTCNGCTC : 660

\* 680 \* 700 \* 720  
LpMDHb : CACAATAAAATGGCGTGNCTTGTGCCATACTGAACTGAACTTGTAAATACCAGAAAGGT : 720

\* 740 \* 760 \* 780  
LpMDHb : GAAACCCGTGCCTATGTACCGACAGTACGGTGAACCCGAAAATCATGAAGGTAGCAGAA : 780

\* 800  
LpMDHb : GATTCTGTGGAAGCTTTCTTTAN : 807

ure 15 Deduced amino acid sequence of LpMDHb

\* 20 \* 40 \* 60  
LpMDHb : LXLLPSEKAVRCHHPXVVRAKTFYAGKANVPVTGVNVPVVGHHAGVTILPQFSQATPASN : 60

\* 80 \* 100 \* 120  
LpMDHb : ALSHEDLKALTAKRTQDGGEVVEAKAGKGSATLSMAYAGAVFGDACLKGNGVPDIVECS : 120

\* 140 \* 160 \* 180  
LpMDHb : FVQSTVTELPPFASKVRLGKNGVEEVIGLGELSAFEKEGLESLKGELEXSIEKGKFAQE : 180

LpMDHb : S : 181

Figure 16 Nucleotide sequences of nucleic acid fragments contributing to the consensus contig sequence LpMDHb

LpMDHb1 :	TTTGGTNCTTTGCCGAG-[NANTAA]-CTGTTGGTGTCAACCACCTTGNGTTGTTCGTGCT	* 20 * 40 * 60	: 60
LpMDHb2 :	-----GCGAGAGAGCTGTTGGTGTCAACCACCTTG[G]GTTGTTCGTGCT		: 44
LpMDHb1 :	AAAACTTCTACGCTGGGAAGGCACACGTGCCAGTCACTGGGGTGAATGTTCTGTTGTTG	* 80 * 100 * 120	: 121
LpMDHb2 :	AAAACTTCTACGCTGGGAAGGCACACGTGCCAGTCACTGGGGTGAATGTTCTGTTGTTG		: 105
LpMDHb1 :	GTGGCCATGCTGGTGTACTATCCTGCCAC[TT]GTTCTCACAGGCTACTCCTGCAAGTAATGC	* 140 * 160 * 180	: 182
LpMDHb2 :	GTGGCCATGCTGGTGTACTATCCTGCCACAGTTCTCACAGGCTACTCCTGCAAGTAATGC		: 166
LpMDHb1 :	ATTGTCCCATGAGGA[CTTAAGGCCCTCACCAAGAGGACACAAGATGGTGGGACGGAAAGTT	* 200 * 220 * 240	: 243
LpMDHb2 :	ATTGTCCCATGAGGA[CTTAAGGCCCTCACCAAGAGGACACAAGATGGTGGGACGGAAAGTT		: 227
LpMDHb1 :	GTTGAAGCAAAGGCTGGAAAGGGCTCAGAACATTGTCATGGCATATGCTGGTGCAGTAT	* 260 * 280 * 300	: 304
LpMDHb2 :	GTTGAAGCAAAGGCTGGAAAGGGCTCAGAACATTGTCATGGCATATGCTGGTGCAGTAT		: 288
LpMDHb1 :	TTGGAGATGCATGCTGAAGGGCTCAATGGAGTTCTGACATTGT[G]AGTGCTCCTTTGT	* 320 * 340 * 360	: 365
LpMDHb2 :	TTGGAGATGCATGCTGAAGGGCTCAATGGAGTTCTGACATTGT[G]AGTGCTCCTTTGT		: 349
LpMDHb1 :	GCAATCAAC[GTAAACAGAGCTGCCATTCTTGCCTCCAAGGTAAGGCTCGGCAAGAACGGA	* 380 * 400 * 420	: 426
LpMDHb2 :	GCAATCAACCGTAACAGAGCTGCCATTCTTGCCTCCAAGGTAAGGCTCGGCAAGAACGGA		: 410
LpMDHb1 :	GTGGAGGAAGTGATTGGGCTGGCGAGCTGTCTGCCTCGAGAAGGA[GGGTCTGGAGAGCC	* 440 * 460 * 480	: 487
LpMDHb2 :	GTGGAGGAAGTGATTGGGCTGGCGAGCTGTCTGCCTCGAGAAGGA[GGGTCTGGAGAGCC		: 471
LpMDHb1 :	TCAAGGGCGAGCTGNCTCCATCGAGAAGGGTATCAAGTTCGCGCAGGAGAGCTAGTC	* 500 * 520 * 540	: 548
LpMDHb2 :	TCAAGGGCGAGCTGT[G]TGTCTCCAT[GAGAAGGGTATCAAGTTCGC]CAGGAGAGCTAGTC		: 532
LpMDHb1 :	AACCTGCTCAGATTCTGACACTCCG[ACATGA]ACTCGGTGGGATCTGATGAATTGGTA	* 560 * 580 * 600 * 620	: 609
LpMDHb2 :	AACCTGCTCAGATTCTAACACTCCG[CACATGA]ACTCGGTGGGATCTGATGAATTGGTA		: 593
LpMDHb1 :	CGACTCCTTC[CTGCCCGTT]TC[G]GGGGACATTGAGGCGT[GNGCT]CACAGTAAAT	* 640 * 660 * 680	: 670
LpMDHb2 :	CGACTCCTTC[ACTGCCCGCTCTGGGGACATTGAGGCGT[GCTCC]CACAAATAAAT		: 654
LpMDHb1 :	GGCGTGN[TTGTTG-CATACTGA]CTGA[CTTNTA]TCTG	* 700 * 720 *	: 708
LpMDHb2 :	GGCGTGT[CTTGTG]GCCATACTGA[ACTGAACTTGTA]ATACCAGAAAGAGTGAAACCTGTGC		: 715

740

760

780

LpMDHb1 : -----  
LpMDHb2 : CTTATGTACCACTACGGTGAACCGAAAATCATGAAGGTAGCAGAAGATTCTGTGGAAG : 776

800

LpMDHb1 : -----  
LpMDHb2 : CTTTTTCTTTAN : 790

Figure 17 Nucleotide sequence of LpMDHc

\* 20 \* 40 \* 60  
LpMDHc : GNNGGTNTACCGAGCGCNCATACTTTNGGTGGAGGTTCTGGACTNGACCCAAGAGAT : 60

\* 80 \* 100 \* 120  
LpMDHc : GTCAATGTTCCCTGTNGNTGGCGGGCATGCCGGAGTTACNATATTGCCACTCCTTCGCAG : 120

\* 140 \* 160 \* 180  
LpMDHc : GTTAATCCTCCCTGCTCATTACCATGAGGAATTAGTATCTCACCTTCACAGCATAACAG : 180

\* 200 \* 220 \* 240  
LpMDHc : AATGGTGGGACAGAAGTNGTCGAGGCAGAAAGCTGGAGCAGGATCGNNACTNTTCTATG : 240

\* 260 \* 280 \* 300  
LpMDHc : GCGNATGCGGCAGCTAAATTGCAGATGCTTGCTNGAGAGGATTGCATGGTATGCTGGG : 300

\* 320 \* 340 \* 360  
LpMDHc : ATAGNGGANTGCTCTTATGTGGATTCTCAGGTGACGGANCTNTCTTNTTGCATCCAAA : 360

\* 380 \* 400 \*  
LpMDHc : GTTCGCCTTGGTTCTGGCGTCNAGGAGATCTGCCACTGGTCCACTAACGAGTN : 419

ure 18 Deduced amino acid sequence of LpMDHc

\* 20 \* 40 \* 60  
LpMDHc : XGXPSXHTXVGEVLGXDP RDVNVPXXGGHAGVXILPLLSQVNPPCSFTMRKLVSHLHSIQ : 60

\* 80 \* 100 \* 120  
LpMDHc : NGGTEXVEAKAGAGSXTXSMAXAAKFADACXRGLHG DAGIXXCSYVDSQVTXXSFASK : 120

\*  
LpMDHc : VRLGCSGVXEILPLGPLNE : 139

Figure 19 Nucleotide sequence of LpMDHd

\* 20 \* 40 \* 60  
LpMDHd : GNGNTTCCGCCAACACAACACCACCGCTCCCCGTCCGCATCTCTCCCTTCGCCCTCAT : 60

\* 80 \* 100 \* 120  
LpMDHd : CGATCCAGATCCCACACACCGCCGCAGCCAGCAACGATGAGGCCGTCGGCGATGAGATCC : 120

\* 140 \* 160 \* 180  
LpMDHd : GCCGCAGCTCCTCCGCCGCCAGCTACTCGTCCGCTCCGCCAGCCGGAGCGGAAG : 180

\* 200 \* 220 \* 240  
LpMDHd : GTGGCCATCCTCGCGCGGCCGGATCGGCAGCCGCTGGCGCTCCTCATGAAGCTG : 240

\* 260 \* 280 \* 300  
LpMDHd : AACCCGCTCGTCTCCTCCCTCTACGACATGCCGCCACCCCGGCCGTCGCCGCC : 300

\* 320 \* 340 \* 360  
LpMDHd : GACGTCTCCCACATCAACTCCCCGGCCCTGGTAAGGGGTTCATGGCGACGATCAGCTC : 360

\* 380 \* 400 \* 420  
LpMDHd : GC GGAGGC GTTGGAGGGGCCGACCTCGTCATCATCCC GGCGTCCGAGGAAGCCC : 420

\* 440 \* 460 \* 480  
LpMDHd : GGCATGACCAGGGACGATCTCTTCAACATCAACGCCGGCATCGTTAAGAACCTCTGCACC : 480

\* 500 \* 520 \* 540  
LpMDHd : GCCATGCCAAGTACTGCCCAACGCTCTTATCAACATGATCAGCAACCCTGTGAACCTCA : 540

\* 560 \* 580 \* 600  
LpMDHd : ACTGTTCCAATTGCTGCTGAAGTTTCAAGAAGGCTGGAACCTATGATGAGAAGAAGTTG : 600

\* 620 \* 640 \* 660  
LpMDHd : TTTGGTGTGACCACTCTGATGTTGTCGTGCCAGGACTTCTATGCTGGAAAGGCTAAT : 660

\* 680 \* 700 \* 720  
LpMDHd : GTACCTGTTACTGGTGTGAACGTTCTGTTGTTGGTGGTATGCTGGTATCACCAATTCTG : 720

\* 740 \* 760 \*  
LpMDHd : CCACTGTTCTCACAGGCAACTCCTCGACTAATGCATTGTCTAGTGAAGACATN : 774

Figure 20 Deduced amino acid sequence of LpMDHd

\* 20 \* 40 \* 60  
LpMDHd : XXPPTQHHRS PVRISP FRLHRSRSHTPP QPATMRPSAMRSAAQLLRRRSYSSASGQPERK : 60

\* 80 \* 100 \* 120  
LpMDHd : VAILGAAGGIGQPL ALLM KLNPLVSSL SLYDIAATPGVAADVSHINS PALVKGF MGDDQL : 120

\* 140 \* 160 \* 180  
LpMDHd : AEALEGADLVII PAGVPRKPGMTRDDL FNINAGIVKNLCTAI AKYCPNALIN MISNPVNS : 180

\* 200 \* 220 \* 240  
LpMDHd : TVPIAAEVFKKAGTYDEK KLFGVTTLDVV RARTFYAGKANP VTGVNV PVVG GHAGITIL : 240

\*  
LpMDHd : PLFSQATPSTNALSSEDX : 258

Figure 21 Nucleotide sequence of LpMDHe

\* 20 \* 40 \* 60  
LpMDHe : TCCGTACNATTGCTGCTGAAGTATTAAAAAAGCTGGGACATACAATCCTAAGAGATTGT : 60

\* 80 \* 100 \* 120  
LpMDHe : TGGGGGTGACAACACTTGATGTAGTGAGAGCCAATACTTTGTGGGTGAGGTTCTGGAC : 120

\* 140 \* 160 \* 180  
LpMDHe : TTGACCCCAGAGATGTCATGTTCCCTGTTGGCGGGCATGCCGGAGTTACGATATTAC : 180

\* 200 \* 220 \* 240  
LpMDHe : CACTCCTTCGCAGGTTAGTCCTCCCTGCTCGTCACCCCTGAGGAAATTAGTTATCTCA : 240

\* 260 \* 280 \* 300  
LpMDHe : CCTCACGCATACAGAATGGTGGGACAGAAGTTGTGGAGGCGAAAGCAGGAGCAGGATCGG : 300

\* 320 \* 340 \* 360  
LpMDHe : CAACTCTTCTATGGCGTATGCGGCAGCTAAATTGAGATGCTTGCTTGAGAGGATTGC : 360

\* 380 \* 400 \* 420  
LpMDHe : ATGGTGATGCTGGGATAGTGGAGTGCTCTTATGTGGATTCTCAGGTGACCGGAACCGCT : 420

\* 440 \* 460 \* 480  
LpMDHe : TCTTTCGCATCCAAAGTTCGCCTAGGTCGTTCTGGCGTCGAGGAGATCTGCAACTGGGT : 480

\* 500 \* 520 \* 540  
LpMDHe : CCACTGAACCAGGTTTGAAAGANCTGGACTGGAANAAGGCAGAAANGAGCTATCCCG : 540

\* 560 \* 580 \* 600  
LpMDHe : AGAGCCTTCCAGAAAGGNTGTGTCATTGTCATGCAACAAAGTGAGTTACATGCCATCATCT : 600

\* 620 \* 640 \* 660  
LpMDHe : TTGTTGGATGTGCTTCCCCAAAGTTCCAACACACCGTCGNAATTGGCATATANATATTGC : 660

\* 680 \* 700 \* 720  
LpMDHe : TGGTTGGGGCCTTGCNTTNATGCAAACAGGCTACCTNTGGTGGGGGGGTCCGTT : 720

\* 740 \* 760 \* 780  
LpMDHe : NTGAAAAAACTCTAACATTTTTACGGTTGGNAACAAAATNTNTGAAAAGCCTGAGA : 780

\* 800 \*  
LpMDHe : ANTATATGATAANTGAANAAAGTTNNNNNNNN : 816

Figure 22 Deduced amino acid sequence of LpMDHe

\* 20 \* 40 \* 60  
LpMDHe : RXIAAEVFKKAGTYNPKRLLGVTTLDVVRANTFVGEVLGLDPRDVNVPVVGHHAGVTILP : 60

\* 80 \* 100 \* 120  
LpMDHe : LLSQVSPPCSFTPEEISYLTTSRIQNGGTEVVEAKAGAGSATLSMAYAAAKFADACLRGLH : 120

\* 140 \* 160 \* 180  
LpMDHe : GDAGIVECSYVDSQVTGTAFFASKVRLGRSGVEEILQLGSTEPGFERXGLEXGEXXSYPE : 180

\* 200 \* 220 \* 240  
LpMDHe : SLPERXCHFXQQSELHAIIFVGCASPKFQHTVXIGIXILLVWGLLXXCKQATXWVGGVRX : 240

\* 260 \*  
LpMDHe : EKLLTFFFXTVNKXXEKPEXYMIXEXXXXX : 271

Figure 23 Consensus contig nucleotide sequence of LpMDHf

\* 20 \* 40 \* 60  
LpMDHf : GGGATGATTNATNCAACAAAAATGCTGGCATTGTCCGATCAATCTGTGAGGGCGTTGCC : 60

\* 80 \* 100 \* 120  
LpMDHf : AAGAGCTGTCCTAATGCAATAGTGAATTGATCAGCAACCCTGTGAACTCAACTGTCCCC : 120

\* 140 \* 160 \* 180  
LpMDHf : ATTGCAGCAGAAGNTTCAAGAGGGCTGGAACCTACTGCCCAAACGTCTCCTGGAGTG : 180

\* 200 \* 220 \* 240  
LpMDHf : ACAACTCTTGATGTAGCGAGGGCTAACACCTTGCTGAAGTGCTGGAGNTGATCCT : 240

\* 260 \* 280 \* 300  
LpMDHf : AGAGAAAGNCAGTGTCCGGNTGTTGGCGGGCATGCAGGGATCACTATATTGCCCTCCTG : 300

\* 320 \* 340 \* 360  
LpMDHf : NCCCAGGTCAGCCCCCGTGCTCATTCACTCCAGATGAAATCAGCTATTGACTAACCGC : 360

\* 380 \* 400 \* 420  
LpMDHf : ATACAGAATGGCGGTACCGAACGTTGAGGCAAAGGCTGGAGCAGGCTCTGCAACTTG : 420

\* 440 \* 460 \* 480  
LpMDHf : TCAATGGCTTTGCTGCTGCAAAATTGCCGATGCATGCTTGCGTGAATCGTGTTGAT : 480

\* 500 \* 520 \* 540  
LpMDHf : GCTGGCATTGTGGAATGTNCATACGTTGCATCTGAGGTGACAGAGCTGCCGTTTTGCA : 540

\* 560 \* 580 \* 600  
LpMDHf : ACAAAAGTGAGGTTAGGTGCGGGAGCTGAGGAGATCCTCCCTGGGCCACTGAAT : 600

\* 620 \* 640 \* 660  
LpMDHf : GACTTGAGAGAGCTGGCCTGGAGAAGGCGAANAAAGGAGCTAGCGAGAGCATCCAGAAG : 660

\* 680 \* 700 \* 720  
LpMDHf : GGTGTGGCGTTCATGAACAAGTGAGATCATATGAATGGATGGATACCCGCAACCTATAAC : 720

\* 740 \* 760 \* 780  
LpMDHf : ATAGATGATGCAAAGACTAAAGAAAGAGTGTGATATAGTGCCTATATACCTGTAAAAT : 780

\*  
LpMDHf : CTCTCCTGCCTGTAAGAA : 798

Figure 24 Deduced amino acid sequence of LpMDHf

\* 20 \* 40 \* 60  
LpMDHf : MLGIVRSICEGVAKSCPNAIVNLISNPVNSTVPIAAEXFKRAGTYCPKRLLGVTTLVAR : 60

\* 80 \* 100 \* 120  
LpMDHf : ANTFVAEVLGXDPREXSVPXVGHHAGITILPLLXQVSPPCSFTPDEISYLTNRIQNGGTE : 120

\* 140 \* 160 \* 180  
LpMDHf : VVEAKAGAGSATLSMAFAAAKFADACLRGMRGDAGIVECXVVADEVTELFFATKVRLGR : 180

\* 200 \* 220  
LpMDHf : GGAEELPLGPLNDFERAGLEKAXKELSESIQKGVAFMNK : 220

Figure 25 Nucleotide sequences of nucleic acid fragments contributing to the consensus contig sequence LpMDHf

LpMDHf1 : GNNNTGATTNATNCACAAAATGCTGGGCATTGTCCGATCAATCTGTGAGGGCGTTGCC LpMDHf2 : -GGATGATTCAACAAAATGCTGGG-ATTGTCCGATCAATCTGTGAGGGCGTTGCC	*            20            *            40            *            60	
LpMDHf1 : AAGAGCTGTCCTAATGCAATAGTGAATTGATCAGCAACCCTGTGAACACTCAACTGTCCCC LpMDHf2 : AAGAGCTGTCCTAATGCAATAGTGAATTGATCAGCAACCCTGTGAACACTCAACTGTCCCC	*            80            *            100            *            120	
LpMDHf1 : ATTGCGGCA <del>AAGNTTTCAAGAGGGCTGGAACCTACTGCCCAAACG</del> TCTCCTTGGAGTG : 180 LpMDHf2 : ATTGCGGCAGAAG <del>TTTCAAGAGGGCTGGAACCTACTGCCCAAACG</del> TCTCCTTGGAGTG : 178	*            140            *            160            *            180	
LpMDHf1 : ACAACTCTTGTAGCGAGGGCTAACACCTTTGCTGAAGTGCTTGAGNTGATCCT : 240 LpMDHf2 : ACAACTCTTGTAGCGAGGGCTAACACCTTTGCTGAAGTGCTTGAGCTTGATCCT	*            200            *            220            *            240	
LpMDHf1 : AGAGAAGNCAGTGTCCGGNTGTTGGCGGGCATGC <del>NGGGATCAGTATATTGCCCTCCTG</del> : 300 LpMDHf2 : AGAGAAG <del>TAGTGTCCGGNTGTTGGCGGGCATGCAGGGATCAGTATATTGCCCTCCTG</del> : 298	*            260            *            280            *            300	
LpMDHf1 : NCCCAGGT <del>CAGCCCCCGTGCCTATTCACTCCAGATGAAATCAGTATTGACTAACCGC</del> : 360 LpMDHf2 : <del>NCCCAGGT<del>CAGCCCCCGTGCCTATTCACTCCAGATGAAATCAGTATTGACTAACCGC</del></del> : 358	*            320            *            340            *            360	
LpMDHf1 : ATACAGAATGGCGGTACCGAAGTTGTTGAGGCAAAGGCTGGAGCAGGCTCTGCAACTTTG : 420 LpMDHf2 : ATACAGAATGGCGGTACCGAAGTTGTTGAGGCAAAGGCTGGAGCAGGCTCTGCAACTTTG : 418	*            380            *            400            *            420	
LpMDHf1 : TCAATGGCTTTGCTGCTGCAAAATT <del>CGCCGATGCATGCTTGCCTGGAATGCCGTGGTGAT</del> : 480 LpMDHf2 : TCAATGGCTTTGCTGCTGCAAAATT <del>CGCCGATGCATGCTTGCCTGGAATGCCGTGGTGAT</del> : 478	*            440            *            460            *            480	
LpMDHf1 : GCTGGCATTGTGGAATGT <del>TACATACGGTGCATCTGAGGTGACAGAGCTGCCGTCTTGCA</del> : 540 LpMDHf2 : GCTGG <del>NATTGTGGAATGT</del> ----- : 497	*            500            *            520            *            540	
LpMDHf1 : ACAAAAGTGAGGTTAGGTCGTGGCGGAGCTGAGGAGATCCTCCCTCTGGGCCACTGAAT : 600 LpMDHf2 : -----	*            560            *            580            *            600	
LpMDHf1 : GACTTTGAGAGAGCTGGCCTGGAGAAGGCGAANAAGGAGCTCAGCGAGAGCATCCAGAAG : 660 LpMDHf2 : -----	*            620            *            640            *            660	
LpMDHf1 : GGTGTGGCGT <del>TCATGAACAAGTGAGATCATATGAATGGATGGATAACCCGCAACCTATAAC</del> : 720 LpMDHf2 : -----	*            680            *            700            *            720	

\* 740 \*

760

\* 780

LpMDHf1 : ATAGATGATGCAAAGACTAAAGAAAGAGTGTGATATAGTGCTCCTATAACCTGTAAAAT : 780  
LpMDHf2 : -----

\*  
LpMDHf1 : CTCTCCCTGCCTGTAAGAA : 798  
LpMDHf2 : -----

Figure 26 Nucleotide sequence of LpMDHg

\* 20 \* 40 \* 60  
LpMDHg : CAATTGCACGTTCTTGCTCACTTCAGCATCACCCCTCACGCTTCTCCTACACAACCCCTCC : 60

\* 80 \* 100 \* 120  
LpMDHg : CAACCGTCACTATGGTCAAGGCTGTCGAGGTGCTGGTGGTACGGCCAGCCCC : 120

\* 140 \* 160 \* 180  
LpMDHg : TCTCTCTTCACTCAAGACGAGCCCCCTCATCGATGAGCTTGCCCTACGATGTTGTCA : 180

\* 200 \* 220 \* 240  
LpMDHg : ACACTCCC GGTTGCCGCTGATCTTCCCACATCTCATCCCGCGCTCAAATGCCGGCT : 240

\* 260 \* 280 \* 300  
LpMDHg : ACCTCCCCAAGGATGATGGCGCAAAGGCTGCATTCAAAGATGCCGACATTATCGTCATCC : 300

\* 320 \* 340 \* 360  
LpMDHg : CCGCCGGCATTCCCTCGCAAGCCTGGCATGACCCGTGATGACCTCTTCAACATCAACGCCG : 360

\* 380 \* 400 \* 420  
LpMDHg : GAATTGTCAAGGGTCTGATTGAGGTTGCCGCCGAAGTTGCCCAAGGCCTTCATTCTGG : 420

\* 440 \* 460 \* 480  
LpMDHg : TCATCTCCAACCCTGTCAACTCTACCGTCCCTATCTTGCCGAGGTCTCAAGGCCAAGG : 480

\* 500 \* 520 \* 540  
LpMDHg : GCGTCTTCAACCCTCAGCGTCTTCGGTGTCAACCACCTCGACATCGTCCGTGCCGAGA : 540

\* 560 \* 580 \* 600  
LpMDHg : CTTTCGTCGCCAGCATCACCGGCGAGAACCGAGCCCCAGAACATTGACCGTCCCCGTATTG : 600

\* 620 \* 640 \* 660  
LpMDHg : GCGGCCACTCCGGCGAGACCATCGTCCCGCTTTCAGCAAGGNTCAGCCCTCTGCTTNCA : 660

LpMDHg : TTCCCGC : 667

Figure 27 Deduced amino acid sequence of LpMDHg

\* 20 \* 40 \* 60  
LpMDHg : IARSCSLQHHPHASPTQPLPTVTMVKAVVAGAAGGIGQPLSLLLKTSPIDEALYDVVN : 60

\* 80 \* 100 \* 120  
LpMDHg : TPGVAADLSHISSRAQIAGYLPKDDGAKAAFKDADIIVIPAGIPRKPGMTRDDLFNINAG : 120

\* 140 \* 160 \* 180  
LpMDHg : IVKGLIEVAAEVAPKAFLVISNPVNSTVPISAEVLKAKGVFPQRLLFGVTTLDIVRAET : 180

\* 200 \* 220  
LpMDHg : FVASITGEKQPQNLTVPIGGHSGETIVPLFSKXQPSAXIP : 221

Figure 28 Consensus contig nucleotide sequence of LpMDHh

LpMDHh :	TNACGGAGCTGCTTAAATCAGCCCCATTCCGCCTCGTCTATAGCGATCCTTCATCCCGT	* 20 * 40 * 60	
LpMDHh :	TGTCGTGCCTCCTCCGAACCACTCTCCCCATCCCCGAACTCCAGAACCGGGCTCCAATG	* 80 * 100 * 120	
LpMDHh :	GCGGGCGAAGGAACCGATGCGCGTGCTCGTCACCGGCCGCAGGACAAATTGGATATGCT	* 140 * 160 * 180	
LpMDHh :	CTTGTCCGATGATTGCTAGGGATTATGCTTGGTGCGGACCAGCCTGTTATTCTGCAT	* 200 * 220 * 240	
LpMDHh :	ATGCTGGATATTCCACCAGCTGCTGAAGCTCTTAATGGTGTAAAGATGGAGTTGGTTGAT	* 260 * 280 * 300	
LpMDHh :	GCCGCATTCACCTCTCAAGGGAGTTGTTGCAACAACTGATGTTGTTGAGGCTTGCACT	* 320 * 340 * 360	
LpMDHh :	GGTGTGAATGTTGCGGTTATGGTTGGATTCCCCAGGAAGGAGGGAAATGGAAAGGAAG	* 380 * 400 * 420	
LpMDHh :	GATGTTATGTCTAAGAATGTTCAATCTACAAATCTCAAGCATCTGCCCTGAAGCCCAT	* 440 * 460 * 480	
LpMDHh :	GCAGCCCCGAATTGCAAGGTTCTGGTTGTTGCCAATCCAGCAAACACCAATGCTCTTATC	* 500 * 520 * 540	
LpMDHh :	TTAAAGGAGTTGCTCCATCTATTCTGAGAAGAACATCAGTTGTTGACCCGCCTAGAC	* 560 * 580 * 600	
LpMDHh :	CATAACAGGGCACTTGGTCAGATCTCTGAGAGACTTGATGTCCAAGTTAGTGATGTGAAG	* 620 * 640 * 660	
LpMDHh :	AATGTTATCATCTGGGCAATCACTCTCCAGTCAGTACCCCTGATGTGAACCACGCCACC	* 680 * 700 * 720	
LpMDHh :	GTGAAGACTTCCAGTGGCGAGAAGCCTGTCAGCTGCAATGGCTAAGACGATGAATGGCTA	* 740 * 760 * 780	
LpMDHh :	AATGCAGGGTTCATGCCACTGTCCAGCAGCGTGGTGCTGCAATCATCAAAGCGAGGAAG	* 800 * 820 * 840	
LpMDHh :	CTCTCCAGTGCTCTCTGCTGCCAGCTGCTGTGACCAATCCGTGATTGGGTTCTC	* 860 * 880 * 900	
LpMDHh :	GGAACCCCTGAGGGAACATTGTTCCATGGGTGTGATTCTGATGGTTCATACGGTGTG	* 920 * 940 * 960	

\* 980 \* 1000 \* 1020  
LpMDHh : CCTGCTGGCTTATCTACTCCTTCCCAGTAAC TGCTGC GGTTGAATGGACAATTGTT : 1020

\* 1040 \* 1060 \* 1080  
LpMDHh : CAAGGGCTCCCGATCGACGAGTTCTCAAGAAAGAAGATGGATGCCACAGCCCAGGAGCTC : 1080

\* 1100 \* 1120 \* 1140  
LpMDHh : TCGGAGGAGAAGGCTCTGCCTACTCGTGCCTCGAGTAAC TGCA ACCAGGGAGCAGCTG : 1140

\* 1160 \* 1180 \* 1200  
LpMDHh : CCGCTCTGATGTTGAATAAAAGGAACATTTGGCTCCATGAAACTCATCTCCACTCAG : 1200

\* 1220 \* 1240 \* 1260  
LpMDHh : AACAGTTGCACATCGCGGTGCCTTAGCTGGTTTCCAGTGTGTATGAATGAGGCTTT : 1260

\* 1280 \* 1300 \* 1320  
LpMDHh : GTAGCTCTATTTCGCCTGATGATTACAGGACAGGATATTGGCAGGAAGATTGGAACAA : 1320

\* 1340 \* 1360 \* 1380  
LpMDHh : TTTGACGTCTGATTAACCAACCTCTTATTATTCCCTGTGTATGAATGAGGCTTTGT : 1380

\* 1400 \* 1420 \* 1440  
LpMDHh : AGCTCTATTTCGCCTGATGATTACAGGCCATGATATTGGCAGGAGGATTGGAACAATT : 1440

\* 1460 \* 1480  
LpMDHh : TGACGCCTGATTAACCAACCTCTTATTACTAAAAAAAAAAAA : 1484

Figure 29 Deduced amino acid sequence of LpMDHh

\* 20 \* 40 \* 60  
LpMDHh : MAAKEPMRVLVTGAAGQIGYALVPMIARGIMLGADQPVILHMLDIPPAAEALNGVKMELV : 60

\* 80 \* 100 \* 120  
LpMDHh : DAAFPLLKGVVATTDVVEACTGVNVAVMVGFFPRKEGMERKDVMMSKNVSIYKSQASALEA : 120

\* 140 \* 160 \* 180  
LpMDHh : HAAPNCVKLVVANPANTNALILKEFAPSPIPEKNISCLTRLDHNRALGQISERLDVQVSDV : 180

\* 200 \* 220 \* 240  
LpMDHh : KNVIIWGNHSSSQYPDVNHATVKTSSGEKPVRELVKDDEWLNAAGFIATVQQRGAAIIKAR : 240

\* 260 \* 280 \* 300  
LpMDHh : KLSSALSAASSACDHIRDWVLGTPEGTFVSMGVYSDGSYGVPAGLIYSFPVTCCGGEWTI : 300

\* 320 \*  
LpMDHh : VQGLPIDEFSRKKMDATAQELSEEKALAYSCLE : 333

Figure 30 Nucleotide sequences of nucleic acid fragments contributing to the consensus contig sequence LpMDHh

	*	20	*	40	*	60	
LpMDHh1	:	TNACGGAGCTGCTTAAATCAGCCCCCATTCGGCCTCGTCT	-	A	C	60	
LpMDHh2	:	GGGNNTTAACCTGT	-	CGNNAN-C	CGTGNCGGT	: 29	
LpMDHh3	:	-	-	GNGTAT	GCNTGNTACA-C	: 24	
LpMDHh4	:	-	-	GTETAACCGTINCTAC	-C	: 22	
LpMDHh5	:	-	-	GNNTAACCHTTC	CCCCGGTTG	: 20	
LpMDHh6	:	-	-	GNNNCCTT	GTCCCGGTTG	: 19	
LpMDHh7	:	-	-	GCTT	CGTATATCCC	: 18	
LpMDHh8	:	-	-	GCTATCCTT	CATCCC	: 19	
LpMDHh9	:	-	-	GCTATCCTT	CATCCC	: 19	
LpMDHh10	:	-	-	NNASCTT	CCNCCC	: 18	
LpMDHh11	:	-	-	NNTEGCT	GTCCC	: 18	
LpMDHh12	:	-	-	CTATCCTT	ATCCC	: 17	
LpMDHh13	:	-	-	GATCCTT	ATCCC	: 16	
LpMDHh14	:	-	-	GNNACTT	GTCCC	: 17	
LpMDHh15	:	-	-	GATCCTT	CATCCC	: 17	
LpMDHh16	:	-	-	GNTCCTT	CATCCC	: 17	
LpMDHh17	:	-	-	GATCCTT	ATCCC	: 16	
LpMDHh18	:	-	-	GNTCC	TCATCCC	: 17	
LpMDHh19	:	-	-	GNNCCTT	CATCCC	: 17	
LpMDHh20	:	-	-	GTTCCTT	NTCCC	: 16	
LpMDHh21	:	-	-	GNTCCTT	CATCCC	: 17	
LpMDHh22	:	-	-	GATCCTT	CATCCC	: 17	
LpMDHh23	:	-	-	GNCCTT	NATCCC	: 16	
LpMDHh24	:	-	-	CNACCTT	NATCCC	: 16	
LpMDHh25	:	-	-	TCCTT	NTCCC	: 16	
LpMDHh26	:	-	-	TCCTT	ATCCC	: 15	
LpMDHh27	:	-	-	ACCTTC	ATCCC	: 15	
LpMDHh28	:	-	-	TCCTT	NTCCC	: 14	
LpMDHh29	:	-	-	TCCTT	ATCCC	: 14	
LpMDHh30	:	-	-	TCCTT	GTCCC	: 15	
LpMDHh31	:	-	-	CCCTT	CATCCC	: 14	
LpMDHh32	:	-	-	NCCTT	GTCCC	: 14	
LpMDHh34	:	-	-	ACCTT	NATCCC	: 14	
LpMDHh35	:	-	-	CTT	GTCCC	: 13	
LpMDHh36	:	-	-	TTNC	GTCCC	: 13	
LpMDHh37	:	-	-	TTNC	GTCCC	: 13	
LpMDHh38	:	-	-	TTT	CATCCC	: 13	
LpMDHh39	:	-	-	TTT	CATCCC	: 12	
LpMDHh40	:	-	-	TTT	ATCCC	: 12	
LpMDHh41	:	-	-	TTT	ATCCC	: 12	
LpMDHh42	:	-	-	TTT	ATCCC	: 12	
LpMDHh43	:	-	-	GTCT	ATCCC	: 12	
LpMDHh44	:	-	-	TT	NTCCC	: 11	
LpMDHh45	:	-	-	TT	GTCCC	: 11	
LpMDHh46	:	-	-	TT	GTCCC	: 11	
LpMDHh47	:	-	-	-	TCCC	: 8	
LpMDHh48	:	-	-	-	CG-TTG	: 5	
LpMDHh49	:	-	-	-	CCGTTG	: 6	
LpMDHh50	:	-	-	-	-	-	
LpMDHh51	:	-	-	-	-	-	
LpMDHh52	:	-	-	-	-	-	
LpMDHh53	:	-	-	-	-	-	
LpMDHh54	:	-	-	-	-	-	
LpMDHh55	:	-	-	-	-	-	
LpMDHh56	:	-	-	-	-	-	
LpMDHh57	:	-	-	-	-	-	
LpMDHh58	:	-	-	-	-	-	
LpMDHh59	:	-	-	-	-	-	
LpMDHh60	:	-	-	-	-	-	
LpMDHh61	:	-	-	-	-	-	
LpMDHh62	:	-	-	-	-	-	
LpMDHh63	:	-	-	-	-	-	
LpMDHh64	:	-	-	-	-	-	

80

100

120







320

340

360

380

400

430







	* 640	* 660	* 680	
LpMDHh1	: GATCTCTGAGAGACTTGATGCCAAGTTAGTGATGTGAANAAATGTTATCATCTGGGGCAATC			: 680
LpMDHh2	: -----			: -
LpMDHh3	: -----			: -
LpMDHh4	: -----			: -
LpMDHh5	: GATCTCTGAGAGACTTGATGCCAAGTTAGTGATGTGAAGAATGTTATCATCTGGGGCAATC			: 640
LpMDHh6	: GATCTCTGAGAGACTTGATGCCAAGTTAGTGATGTGAAGAATGTTATCATCTGGGGCAATC			: 638
LpMDHh7	: GATCTCTGAGAGACTTNTATGCCAANTTAGTGATGTGAANAAATGTTATCATCTGGGGTAATC			: 636
LpMDHh8	: GATCTCTGAGAGACTTGATGCCAAGTTAGTGATGTGAAGAATGTTATCATCTGGGGCAATC			: 639
LpMDHh9	: GATCTCTGAGAGACTTGATGTCCAAGTTAGTGATGTGAAGAATGTTATCATCTGGGGCAATC			: 639
LpMDHh10	: GATCTCTGAGAGACTTGATGCCAAGTTAGTGATGTGAAGAATGTTATCATCTGGGGCAATC			: 637
LpMDHh11	: GATCTCTGAGAGACTTGATGCCAAGTTAGTGATGTGAAGAATGTTATCATCTGGGGCAATC			: 638
LpMDHh12	: GATCTCTGAGAGACTTGATGCCAAGTTAGTGATGTGAAGAATGTTATCATCTGGGGCAATC			: 636
LpMDHh13	: -----			: -
LpMDHh14	: GATCTCTGAGAGACTTGATGCCAAGTTAGTGATGTGAAGAATGTTATCATCTGGGGTAATC			: 636
LpMDHh15	: GATCTCTGAGAGACTTGATGCCAAGTTAGTGATGTGAAGAATGTTATCATCTGGGGCAATC			: 636
LpMDHh16	: GATCTCTGAGAGGCTTGATGTCCAAGTTAGTGATGTGAAGAATGTTATCATCTGGGGTAATC			: 636
LpMDHh17	: GATCTCTGAGAGACTTGATGTCCAAGTTAGTGATGTGAAGAATGTTATCATCTGGGGCAATC			: 635
LpMDHh18	: GATCTCTGAGAGACTTGATGCCAAGTTAGTGATGTGAAGAATGTTATCATCTGGGGTAATC			: 636
LpMDHh19	: GATCTCTGAGAGACTTGATGCCAAGTTAGTGATGTGAAGAATGTTATCATCTGGGGCAATC			: 636
LpMDHh20	: GATCTCTGAGAGGCTTGATGTCCAAGTTAGTGATGTGAAGAATGTTATCATCTGGGGTAATC			: 635
LpMDHh21	: GATCTCTGAGAGACTTGATGTCCAAGTTAGTGATGTGAAGAATGTTATCATCTGGGGCAATC			: 636
LpMDHh22	: GATCTCTGAGAGACTTGATGCCAAGTTAGTGATGTGAAGAATGTTATCATCTGGGGCAATC			: 636
LpMDHh23	: -----			: -
LpMDHh24	: -----			: -
LpMDHh25	: GATCTCTGAGAGACTTGATGTGCCAAGTTAGTGAAANAAATGTTATCATCTGGGGCAATC			: 635
LpMDHh26	: GATCTCTGAGAGACTTGATGTCCAAGTTAGTGATGTGAAGAATGTTATCATCTGGGGCAATC			: 634
LpMDHh27	: GATCTCTGAGAGACTTGATGTCCAAGTTAGTGATGTGAAGAATGTTATCATCTGGGGTAATC			: 635
LpMDHh28	: GATCTCTGAGAGACTTGATGTCCAAGTTAGTGATGTGAAGAATGTTATCATCTGGGGCAATC			: 633
LpMDHh29	: GATCTCTGAGAGACTTGATGTCCAAGTTAGTGATGTGAAGAATGTTATCATCTGGGGCAATC			: 633
LpMDHh30	: GATCTCTGAGAGGCTTGATGTCCAAGTTAGTGATGTGAAGAATGTTATCATCTGGGGTAATC			: 634
LpMDHh31	: AATCTTNAAGACTTGNTNTCAAN-----			: 595
LpMDHh32	: GATCTCTGAGAGACTTGATGTCCAAGTTAGNGATGNGAAANAAATGTTATCATCTGGGGCAATC			: 634
LpMDHh34	: GATCTCTGAGAGACTTGATGTCCAAGTTAGTGATGTGAAGAATGTTATCATCTGGGGCAATC			: 633
LpMDHh35	: -----			: -
LpMDHh36	: GATCTCTGAAAGACTTGATGTCCAAGTTA-----			: 599
LpMDHh37	: GATCTCTGAGAGACTTGATGTCCAAGTTAGTGATG-----			: 606
LpMDHh38	: GATCTCTGAGAGACTTGATGTCCAAGTTAGTGATGTGAAGAATGTTATCATCTGGGGCAATC			: 631
LpMDHh39	: -----			: -
LpMDHh40	: -----			: -
LpMDHh41	: GAATCTCTGAGAGACNTGATGCCAAGNTNGNGNTGN-----			: 605
LpMDHh42	: GATCTCTGAGAGACTTGATGTCCAAGTTAGTGATGTGAAGAATGTTATCATCTGGGGCAATC			: 630
LpMDHh43	: GATCTCTGAGAGACTTGATGTCCAAGTTAGTGATGTGAAGAATGTTATCATCTGGGGCAATC			: 631
LpMDHh44	: GATCTCTGAGAGACTTGATGTCCAAGTTAGTGATGTGAAGAATGTTATCATCTGGGGCAATC			: 630
LpMDHh45	: GATCTCTGAGAGACTTGATGTCCAAGTTAGTGATGTGAAGAATGTTATCATCTGGGGTAATC			: 629
LpMDHh46	: GATCTCTGAGAGACTTGATGTCCAAGTTAGTGATGTGAAGAATGTTATCATCTGGGGTAATC			: 630
LpMDHh47	: GATCTTGAGAGACTTGATGCCAAGTTAGTGATGTGAAGAATGTTATCATCTGGGGCAATC			: 627
LpMDHh48	: GATCTCTGAGAGACTTGATGTCCAAGTTAGTGATGTGAAGAATGTTATCATCTGGGGCAATC			: 623
LpMDHh49	: GATCTCTGAGAGACTTGATGTCCAAGTTAGTGATGTGAAGAATGTTATCATCTGGGGCAATC			: 626
LpMDHh50	: GATCTCTGAGAGACTTGATGTCCAAGTTAGTGATGTGAAGAATGTTATCATCTGGGGCAATC			: 604
LpMDHh51	: GATCTCTGAGAGACTTGATGTCCAAGTTAGTGATGTGAAGAATGTTATCATCTGGGGTAATC			: 587
LpMDHh52	: GATCTCTGAGAGACTTGATGTCCAAGTTAGTGATGTGAAGAATGTTATCATCTGGGGCAATC			: 553
LpMDHh53	: GATCTCTGAGAGACTTGATGTGCCAAGTTAGTGATGTGAANAAATGNTATCATCTGGNCAGTC			: 475
LpMDHh54	: GATCTCTGAGAGACTTGATGTCCAAGTTAGTGATGTGAAGAATGTTATCATCTGGGGCAATC			: 304
LpMDHh55	: GATCTCTGAGAGACTTGATGTCCAAGTTAGTGATGTGAAGAATGTTATCATCTGGGGTAATC			: 226
LpMDHh56	: GATCTCTGAGAGACTTGATGTCCAAGTTAGTGATGTGAAGAATGTTATCATCTGGGGCAATC			: 206
LpMDHh57	: GATCTCTGAGAGACTTGATGTCCAAGTTAGTGATGTGAAGAATGTTATCATCTGGGGCAATC			: 202
LpMDHh58	: -----GCAATC			: 6
LpMDHh59	: -----			: -
LpMDHh60	: -----			: -
LpMDHh61	: -----			: -
LpMDHh62	: -----			: -
LpMDHh63	: -----			: -
LpMDHh64	: -----			: -

	* 700	* 720	* 740	
LpMDHh1	: ACTCTTNCAGTCAGTACCCCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGCGAGAAG			: 742
LpMDHh2	: -----			
LpMDHh3	: -----			
LpMDHh4	: -----			
LpMDHh5	: ACTCTTCCAG-----			: 650
LpMDHh6	: ACTCTTCCAGTCAGTACCCCTGA-----			: 660
LpMDHh7	: ACTCTTCCAGTCATAACCTGATGTGAACCACGCCNNAAANACTTCCAGGGCGA-----			: 693
LpMDHh8	: ACTCTTCCAGTCAGTACCCCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGGCGAGAAG			
LpMDHh9	: ACTCTTCCAGTCAGTACCCCTGATGTGAACCACGCCACCGTGAAGACTTCCAGGGCGAGAAG			: 701
LpMDHh10	: ACTCTTCCAGTCAGTACCCCTGATGTGAACCACGCCACCGTGAAGACTTCCAGGGCGAGAAG			: 701
LpMDHh11	: ACTCTTCCAGTCAGTACCCCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGGCGAGAAG			: 684
LpMDHh12	: ACTCTTCCAGTCAGTACCCCTGATGTGAACCACGCCACCGTGAAGACTTNCAGTGGCGAGAAG			: 700
LpMDHh13	: -----			: 698
LpMDHh14	: ACTCTTCCAGTCATAACCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGGN-----			
LpMDHh15	: ACTCTTCCAGTCAGTACCCCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGGCGAGAAG			: 692
LpMDHh16	: ACTCTTCCAGTCATAACCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGGCGAGAAG			: 698
LpMDHh17	: ACTCTTCCAGTCAGTACCCCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGGCGAGAAG			: 698
LpMDHh18	: ACTCTTCCAGTCATAACCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGGCGAGAAG			: 697
LpMDHh19	: ACTCTTNCAGTCAGTACCCCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGGCGAGAAG			: 698
LpMDHh20	: ACTCTTCCAGTCATAACCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGGCGAGAAG			: 698
LpMDHh21	: ACTCTTCCAGTCAGTACCCCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGGCGAGAAG			: 697
LpMDHh22	: ACTCTTCCAGTCAGTACCCCTGATGTGAACCACGCCACCGTGAAGACTTNCAGTGGCGAGAAG			: 698
LpMDHh23	: -----			: 698
LpMDHh24	: -----			
LpMDHh25	: ACTCTTNCAGNCATAACCTGATGTGAACCACGCCACCGNGAACAGACTNTCACTGCCNAAG			
LpMDHh26	: ACTCTTCCAGTC-----			: 696
LpMDHh27	: ACTCTTNCAGTCATAACCTGATGTGAACCACGCCACCGTGAANACTTNCAGTGGCGAGAAG			: 646
LpMDHh28	: ACTCTTCCAGTCAGTACCCCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGGCGAGAAG			: 697
LpMDHh29	: ACTCTTCCAGTCAGTACCCCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGGCGAGAAG			: 695
LpMDHh30	: ACTCTTCCAGTCATAACCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGGCGAGAAG			: 695
LpMDHh31	: -----			: 696
LpMDHh32	: ACTCTTCCAGTCAGTACCCCTGATGTGAACCACGCCACCGNGAACAGACTTCCAGTGNCGAGAAG			
LpMDHh34	: ACTCTTCCAGTCAGTACCCCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGGCGAGAAG			: 696
LpMDHh35	: -----			: 695
LpMDHh36	: -----			
LpMDHh37	: -----			
LpMDHh38	: ACTCTTCCAGTCAGTACCCCTGATGTGAACCACGCCACCGTGAAGACTTNCAGTGGCGAGAAG			: 686
LpMDHh39	: -----			
LpMDHh40	: -----			
LpMDHh41	: -----			
LpMDHh42	: ACTCTTCCAGTCAGTACCCCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGG-----			: 685
LpMDHh43	: ACTCTTCCAGTCAGTACCCCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGGCGAGAAG			: 693
LpMDHh44	: ACTCTTCCAGTCAGTACCCCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGGCGAGAAG			: 692
LpMDHh45	: ACTCTTCCAGTCATAACCTGATGTGAACCACGCCACCGTGAAGACTTNCAGTGGCGAGAAG			: 690
LpMDHh46	: ACTCTTCCAGTCATAACCTGATGTGAACCACGCCACCGTGAAGACTTNCAGTGGCGAGAAG			: 692
LpMDHh47	: ACTNTTCCAGTCAGTNCCCTGATGTGAACCACNCCTCCCGAAAANACTTCCAG-----			: 679
LpMDHh48	: ACTCTTCCAGTCAGTACCCCTGATGTGAACCACGCCACCGTGAAGACTTCCAG-----			: 676
LpMDHh49	: ACTCTTCCAGTCAGTACCCCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGGCGAGAAG			: 688
LpMDHh50	: ACTCTTCCAGTCAGTACCCCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGGCGAGAAG			: 666
LpMDHh51	: ACTCTTCCAGTCATAACCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGGCGAGAAG			: 649
LpMDHh52	: ACTCTTCCAGTCAGTACCCCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGGCGAGAAG			: 615
LpMDHh53	: ACTCTTNCANNCNATNCCTGATGTGNNANCCNCGCCACG-----			: 513
LpMDHh54	: ACTCTTCCAGTCAGTACCCCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGGCGAGAAG			: 366
LpMDHh55	: ACTCTTCCAGTCATAACCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGGCGAGAAG			: 288
LpMDHh56	: ACTCTTCCAGTCAGTACCCCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGGCGAGAAG			: 268
LpMDHh57	: ACTCTTCCAGTCAGTACCCCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGGCGAGAAG			: 264
LpMDHh58	: ACTCTTCCAGTCAGTACCCCTGNTGAACCACGCCACCGTGAAGACTTCCAGTGGCGAGAAG			: 67
LpMDHh59	: -----GTACCCCTGATGTGAACCACGCCACCGTGAAGACTTCCAGTGGCGAGAAG			: 49
LpMDHh60	: -----TMCNGTGGCAAGAG-----			: 14
LpMDHh61	: -----GCGAGAAG			: 8
LpMDHh62	: -----			
LpMDHh63	: -----			
LpMDHh64	: -----			

	* 760 * 780 *	800	
LpMDHh1	CCTGTTCGCGAACTTGTAAAGACGATG		770
LpMDHh2	-		-
LpMDHh3	-		-
LpMDHh4	-		-
LpMDHh5	-		-
LpMDHh6	-		-
LpMDHh7	-		-
LpMDHh8	CCTGTTCGCGAACTTGTAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA		763
LpMDHh9	CCTGTTCGCGAACTTGTAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA		763
LpMDHh10	-		-
LpMDHh11	CCTGTT-		707
LpMDHh12	CCTGTTCGCGAACTTGTAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA		760
LpMDHh13	-		-
LpMDHh14	-		-
LpMDHh15	CCTGTTCGCGAACTTGTAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA		760
LpMDHh16	CCTGTTCGCGAACTTGTAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA		760
LpMDHh17	CCTGTTCGCGAACTTGTAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA		759
LpMDHh18	CCTGTTCGCGAACTTGTAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA		759
LpMDHh19	CCTGTTCGCGAACTTGTAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA		760
LpMDHh20	CCTGTTCGCGAACTTGTAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA		760
LpMDHh21	CCTGTTCGCGAACTTGTAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA		759
LpMDHh22	CCTGTTCGCGAACTTGTAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA		760
LpMDHh23	-		-
LpMDHh24	-		-
LpMDHh25	-		-
LpMDHh26	-		-
LpMDHh27	CCTGTTCGCGAACT-		711
LpMDHh28	CCTGTTCGCGAACTTGTAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA		757
LpMDHh29	CCTGTTCGCGAACTTGTAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA		757
LpMDHh30	CCTGTTCGCGAACTTGTAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA		758
LpMDHh31	-		-
LpMDHh32	-		-
LpMDHh34	CCTGTTCGCGAACTTGTAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA		757
LpMDHh35	-		-
LpMDHh36	-		-
LpMDHh37	-		-
LpMDHh38	-		-
LpMDHh39	-		-
LpMDHh40	-		-
LpMDHh41	-		-
LpMDHh42	-		-
LpMDHh43	CCTGTTCGCGAACTTGTAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA		755
LpMDHh44	CCTGTTCGCGAACTTGTAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA		754
LpMDHh45	-		-
LpMDHh46	CCTGTTCG-		700
LpMDHh47	-		-
LpMDHh48	-		-
LpMDHh49	CCTGTTCGCGAACTTGTAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA		750
LpMDHh50	CCTGTTCGCGAACTTGTAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA		728
LpMDHh51	CCTGTTCGCGAACTTGTAAAGACGAT-		676
LpMDHh52	CCTGTTCGCGAACTTGTAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA		677
LpMDHh53	-		-
LpMDHh54	CCTGTTCGCGAACTTGTAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA		428
LpMDHh55	CCTGTTCGCGAACTTGTAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA		350
LpMDHh56	CCTGTTCGCGAACTTGTAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA		330
LpMDHh57	CCTGTTCGCGAACTTGTAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA		326
LpMDHh58	CCTGTTCGCGAACTTGTAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA		129
LpMDHh59	CCTGTTCGCGAACTTGTAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA		111
LpMDHh60	CCTGTTCGCGAACTTGTAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA		75
LpMDHh61	CCTGTTCGCGAACTTGTAAAGACGATGAATGGCTAAATGCAGGGTTCATTGCCACTGTCCA		70
LpMDHh62	-		-
LpMDHh63	-		-
LpMDHh64	-		-

	*	820	*	840	*	860	
LpMDHh1	:	-					-
LpMDHh2	:	-					-
LpMDHh3	:	-					-
LpMDHh4	:	-					-
LpMDHh5	:	-					-
LpMDHh6	:	-					-
LpMDHh7	:	-					-
LpMDHh8	:	GCAGCGTGGTGCTGCAATCATCAAAGCGAG-					793
LpMDHh9	:	GCAGCGTGGNGCTGCAATCATCAAAGNGAGGAAC					797
LpMDHh10	:	-					-
LpMDHh11	:	-					-
LpMDHh12	:	GCAGCGTGGTGCTGCAATCATCAAAGCGAGGAAGCTCTNC					801
LpMDHh13	:	-					-
LpMDHh14	:	-					-
LpMDHh15	:	GCAG-					764
LpMDHh16	:	GCAGCGTGG-					769
LpMDHh17	:	GCANCGTGGTG-					770
LpMDHh18	:	GCAGCGTGGTGCTGCAATC					779
LpMDHh19	:	ACAGCGTGGTGCTGCAATCATCAAAGCG					788
LpMDHh20	:	GCAGCGTGGTGCTGCAATCATCAAAGCGAGGAAGC					794
LpMDHh21	:	GCAGCGTGGTGCTGCNATCATCAAAGCGAGGAAGCT					797
LpMDHh22	:	GCAGCGTGGNGCTGCATCATCAAAGCGAGGAAGCTCTCAGT					802
LpMDHh23	:	-					-
LpMDHh24	:	-					-
LpMDHh25	:	-					-
LpMDHh26	:	-					-
LpMDHh27	:	-					-
LpMDHh28	:	GCAGCGTGGTG-					768
LpMDHh29	:	GCAGCGTGGTGCTGCAATCATCAAAG					783
LpMDHh30	:	GCAGCGTGGTGCTGCAATCATCAAAGCGAGGAAGCTCTNCAGTGC					803
LpMDHh31	:	-					-
LpMDHh32	:	-					-
LpMDHh34	:	GCAGCGTGGTGCTGCAATCATCA					779
LpMDHh35	:	-					-
LpMDHh36	:	-					-
LpMDHh37	:	-					-
LpMDHh38	:	-					-
LpMDHh39	:	-					-
LpMDHh40	:	-					-
LpMDHh41	:	-					-
LpMDHh42	:	-					-
LpMDHh43	:	GCAGCGTGG-					763
LpMDHh44	:	GCAGCGTGGTGCTGCAATCATCAAAGCGAGGAAGCT					790
LpMDHh45	:	-					-
LpMDHh46	:	-					-
LpMDHh47	:	-					-
LpMDHh48	:	-					-
LpMDHh49	:	GCAGCGTGGTGCTGCAATCATCAAAGCGAGGAAGCT					786
LpMDHh50	:	GCAGCGTGGTGCTGCAATCATCAAAGCGAGGAAGCTCTCCAGTG					772
LpMDHh51	:	-					-
LpMDHh52	:	GCAGCGTGGTGCTGCAATCATCAAAGCGAGGAAGCTCTCCAGTGCTCTCTGCTGCCAGCT					739
LpMDHh53	:	-					-
LpMDHh54	:	GCAGCGTGGTGCTGCAATCATCAAAGCGAGGAAGCTCTCCAGTGCTCTCTGCTGCCAGCT					490
LpMDHh55	:	GCAGCGTGGTGCTGCAATCATCAAAGCGAGGAAGCTCTCCAGTGCTCTCTGCTGCCAGCT					412
LpMDHh56	:	GCAGCGTGGTGCTGCAATCATCAAAGCGAGGAAGCTCTCCAGTGCTCTCTGCTGCCAGCT					392
LpMDHh57	:	GCAGCGTGGTGCTGCAATCATCAAAGCGAGGAAGCTCTCCAGTGCTCTCTGCTGCCAGCT					388
LpMDHh58	:	GCAGCGTGGTGCTGCAATCATCAAAGCGAGGAAGCTCTCCAGTGCTCTCTGCTGCCAGCT					191
LpMDHh59	:	GCAGCGTGGTGCTGCAATCATCAAAGCGAGGAAGCTCTCCAGTGCTCTCTGCTGCCAGCT					173
LpMDHh60	:	GCAGCGTGGTGCTGCAATCATCAAAGCGAGGAAGCTCTCCAGTGCTCTCTGCTGCCAGCT					137
LpMDHh61	:	GCAGCGTGGTGCTGCAATCATCAAAGCGAGGAAGCTCTCCAGTGCTCTCTGCTGCCAGCT					132
LpMDHh62	:	-					-
LpMDHh63	:	-					-
LpMDHh64	:	-					-

	*	880	*	900	*	920	*
LpMDHh1	:	-	-	-	-	-	-
LpMDHh2	:	-	-	-	-	-	-
LpMDHh3	:	-	-	-	-	-	-
LpMDHh4	:	-	-	-	-	-	-
LpMDHh5	:	-	-	-	-	-	-
LpMDHh6	:	-	-	-	-	-	-
LpMDHh7	:	-	-	-	-	-	-
LpMDHh8	:	-	-	-	-	-	-
LpMDHh9	:	-	-	-	-	-	-
LpMDHh10	:	-	-	-	-	-	-
LpMDHh11	:	-	-	-	-	-	-
LpMDHh12	:	-	-	-	-	-	-
LpMDHh13	:	-	-	-	-	-	-
LpMDHh14	:	-	-	-	-	-	-
LpMDHh15	:	-	-	-	-	-	-
LpMDHh16	:	-	-	-	-	-	-
LpMDHh17	:	-	-	-	-	-	-
LpMDHh18	:	-	-	-	-	-	-
LpMDHh19	:	-	-	-	-	-	-
LpMDHh20	:	-	-	-	-	-	-
LpMDHh21	:	-	-	-	-	-	-
LpMDHh22	:	-	-	-	-	-	-
LpMDHh23	:	-	-	-	-	-	-
LpMDHh24	:	-	-	-	-	-	-
LpMDHh25	:	-	-	-	-	-	-
LpMDHh26	:	-	-	-	-	-	-
LpMDHh27	:	-	-	-	-	-	-
LpMDHh28	:	-	-	-	-	-	-
LpMDHh29	:	-	-	-	-	-	-
LpMDHh30	:	-	-	-	-	-	-
LpMDHh31	:	-	-	-	-	-	-
LpMDHh32	:	-	-	-	-	-	-
LpMDHh34	:	-	-	-	-	-	-
LpMDHh35	:	-	-	-	-	-	-
LpMDHh36	:	-	-	-	-	-	-
LpMDHh37	:	-	-	-	-	-	-
LpMDHh38	:	-	-	-	-	-	-
LpMDHh39	:	-	-	-	-	-	-
LpMDHh40	:	-	-	-	-	-	-
LpMDHh41	:	-	-	-	-	-	-
LpMDHh42	:	-	-	-	-	-	-
LpMDHh43	:	-	-	-	-	-	-
LpMDHh44	:	-	-	-	-	-	-
LpMDHh45	:	-	-	-	-	-	-
LpMDHh46	:	-	-	-	-	-	-
LpMDHh47	:	-	-	-	-	-	-
LpMDHh48	:	-	-	-	-	-	-
LpMDHh49	:	-	-	-	-	-	-
LpMDHh50	:	-	-	-	-	-	-
LpMDHh51	:	-	-	-	-	-	-
LpMDHh52	:	CTGCTTGTGACCACATCCGTGATT	-	-	-	-	763
LpMDHh53	:	-	-	-	-	-	-
LpMDHh54	:	CTGCTTGTGACCACATCCGGATTGGGTTCTCGGAACCCCTGAGGAAACATTGTTCCATG	-	-	-	-	552
LpMDHh55	:	CTGCTTGTGACCACATCCGTGATTGGGTTCTCGGAACCCCTGAGGAAACATTGTTCCATG	-	-	-	-	474
LpMDHh56	:	CTGCTTGTGACCACATCCGTGATTGGGTTCTCGGAACCCCTGAGGAAACATTGTTCCATG	-	-	-	-	454
LpMDHh57	:	CTGCTTGTGACCACATCCGTGATTGGGTTCTCGGAACCCCTGAGGAAACATTGTTCCATG	-	-	-	-	450
LpMDHh58	:	CTGCTTGTGACCACATCCGTGATTGGGTTCTCGGAACCCCTGAGGAAACATTGTTCCATG	-	-	-	-	253
LpMDHh59	:	CTGCTTGTGACCACATCCGTGATTGGGTTCTCGGAACCCCTGAGGAAACATTGTTCCATG	-	-	-	-	235
LpMDHh60	:	CTGCTTGTGACCACATCCGTGATTGGGTTCTCGGAACCCCTGAGGAAACATTGTTCCATG	-	-	-	-	199
LpMDHh61	:	CTGCTTGTGACCACATCCGTGATTGGGTTCTCGGAACCCCTGAGGAAACATTGTTCCATG	-	-	-	-	194
LpMDHh62	:	-	-	-	-	-	-
LpMDHh63	:	-	-	-	-	-	-
LpMDHh64	:	-	-	-	-	-	-

940

\*

960

\*

980

\*

LpMDHh1	:	-	-	-	-
LpMDHh2	:	-	-	-	-
LpMDHh3	:	-	-	-	-
LpMDHh4	:	-	-	-	-
LpMDHh5	:	-	-	-	-
LpMDHh6	:	-	-	-	-
LpMDHh7	:	-	-	-	-
LpMDHh8	:	-	-	-	-
LpMDHh9	:	-	-	-	-
LpMDHh10	:	-	-	-	-
LpMDHh11	:	-	-	-	-
LpMDHh12	:	-	-	-	-
LpMDHh13	:	-	-	-	-
LpMDHh14	:	-	-	-	-
LpMDHh15	:	-	-	-	-
LpMDHh16	:	-	-	-	-
LpMDHh17	:	-	-	-	-
LpMDHh18	:	-	-	-	-
LpMDHh19	:	-	-	-	-
LpMDHh20	:	-	-	-	-
LpMDHh21	:	-	-	-	-
LpMDHh22	:	-	-	-	-
LpMDHh23	:	-	-	-	-
LpMDHh24	:	-	-	-	-
LpMDHh25	:	-	-	-	-
LpMDHh26	:	-	-	-	-
LpMDHh27	:	-	-	-	-
LpMDHh28	:	-	-	-	-
LpMDHh29	:	-	-	-	-
LpMDHh30	:	-	-	-	-
LpMDHh31	:	-	-	-	-
LpMDHh32	:	-	-	-	-
LpMDHh34	:	-	-	-	-
LpMDHh35	:	-	-	-	-
LpMDHh36	:	-	-	-	-
LpMDHh37	:	-	-	-	-
LpMDHh38	:	-	-	-	-
LpMDHh39	:	-	-	-	-
LpMDHh40	:	-	-	-	-
LpMDHh41	:	-	-	-	-
LpMDHh42	:	-	-	-	-
LpMDHh43	:	-	-	-	-
LpMDHh44	:	-	-	-	-
LpMDHh45	:	-	-	-	-
LpMDHh46	:	-	-	-	-
LpMDHh47	:	-	-	-	-
LpMDHh48	:	-	-	-	-
LpMDHh49	:	-	-	-	-
LpMDHh50	:	-	-	-	-
LpMDHh51	:	-	-	-	-
LpMDHh52	:	-	-	-	-
LpMDHh53	:	-	-	-	-
LpMDHh54	:	GGTGTGTATTCTGATGGNTATACNGGGTGCCTGGCTGGGTTATCTACTCCTTCCAGNAAC	:	613	
LpMDHh55	:	GGTGTGTATTCTGATGGTCATACGGTGTGCCTGCTGGGTTATCTACTCCTTCCCAGTAAC	:	536	
LpMDHh56	:	GNTGTGTATTCTGATGGTCATACGGTGTGCCTGCTGGGTTATCTACTCCTTCCCAGTAAC	:	516	
LpMDHh57	:	GGTGTGTATTCTGATGGTCATACGGTGTGCCTGCTGGGTTATCTACTCCTTCCCAGTAAC	:	512	
LpMDHh58	:	GGTGTGTATTCTGATGGTCATACGGTGTGCCTGCTGGGTTATCTACTCCTTCCCAGTAAC	:	315	
LpMDHh59	:	GGTGTGTATTCTGATGGTCATACGGTGTGCCTGCTGGGTTATCTACTCCTTCCCAGTAAC	:	297	
LpMDHh60	:	GGTGTGTATTCTGATGGTCATACGGTGTGCCTGCTGGGTTATCTACTCCTTCCCAGTAAC	:	261	
LpMDHh61	:	GGTGTGTATTCTGATGGTCATACGGTGTGCCTGCTGGGTTATCTACTCCTTCCCAGTAAC	:	256	
LpMDHh62	:	-	-	-	
LpMDHh63	:	-	-	-	
LpMDHh64	:	-	-	-	

	1000	*	1020	*	1040	*	
LpMDHh1	:	-	-	-	-	-	
LpMDHh2	:	-	-	-	-	-	
LpMDHh3	:	-	-	-	-	-	
LpMDHh4	:	-	-	-	-	-	
LpMDHh5	:	-	-	-	-	-	
LpMDHh6	:	-	-	-	-	-	
LpMDHh7	:	-	-	-	-	-	
LpMDHh8	:	-	-	-	-	-	
LpMDHh9	:	-	-	-	-	-	
LpMDHh10	:	-	-	-	-	-	
LpMDHh11	:	-	-	-	-	-	
LpMDHh12	:	-	-	-	-	-	
LpMDHh13	:	-	-	-	-	-	
LpMDHh14	:	-	-	-	-	-	
LpMDHh15	:	-	-	-	-	-	
LpMDHh16	:	-	-	-	-	-	
LpMDHh17	:	-	-	-	-	-	
LpMDHh18	:	-	-	-	-	-	
LpMDHh19	:	-	-	-	-	-	
LpMDHh20	:	-	-	-	-	-	
LpMDHh21	:	-	-	-	-	-	
LpMDHh22	:	-	-	-	-	-	
LpMDHh23	:	-	-	-	-	-	
LpMDHh24	:	-	-	-	-	-	
LpMDHh25	:	-	-	-	-	-	
LpMDHh26	:	-	-	-	-	-	
LpMDHh27	:	-	-	-	-	-	
LpMDHh28	:	-	-	-	-	-	
LpMDHh29	:	-	-	-	-	-	
LpMDHh30	:	-	-	-	-	-	
LpMDHh31	:	-	-	-	-	-	
LpMDHh32	:	-	-	-	-	-	
LpMDHh34	:	-	-	-	-	-	
LpMDHh35	:	-	-	-	-	-	
LpMDHh36	:	-	-	-	-	-	
LpMDHh37	:	-	-	-	-	-	
LpMDHh38	:	-	-	-	-	-	
LpMDHh39	:	-	-	-	-	-	
LpMDHh40	:	-	-	-	-	-	
LpMDHh41	:	-	-	-	-	-	
LpMDHh42	:	-	-	-	-	-	
LpMDHh43	:	-	-	-	-	-	
LpMDHh44	:	-	-	-	-	-	
LpMDHh45	:	-	-	-	-	-	
LpMDHh46	:	-	-	-	-	-	
LpMDHh47	:	-	-	-	-	-	
LpMDHh48	:	-	-	-	-	-	
LpMDHh49	:	-	-	-	-	-	
LpMDHh50	:	-	-	-	-	-	
LpMDHh51	:	-	-	-	-	-	
LpMDHh52	:	-	-	-	-	-	
LpMDHh53	:	-	-	-	-	-	
LpMDHh54	:TTGCTGNGGGGGAAATGGACAATTGNTCAAAGGCTNCCNATCNACNAGTT-					: 664	
LpMDHh55	:TTGCTCGGTGGTGAATGGACAATTGTTCAAGGGCTCCCGATCGACGAGTTCTCAAGAAAGA					: 598	
LpMDHh56	:TTGCTCGGTGGTGAATGGACAATTGTTCAAGGGCTCCCGATCGACGAGTTCTCAAGAAAGA					: 578	
LpMDHh57	:TTGCTCGGTGGTGAATGGACAATTGTTCAAGGGCTCCCGATCGACGAGTTCTCAAGAAAGA					: 574	
LpMDHh58	:TTGCTCGGTGGTGAATGGACAATTGTTCAAGGGCTCCCGATCGACGAGTTCTCAAGAAAGA					: 377	
LpMDHh59	:TTGCTCGGTGGTGAATGGACAATTGTTCAAGGGCTCCCGATCGACGAGTTCTCAAGAAAGA					: 359	
LpMDHh60	:TTGCTCGGTGGTGAATGGACAATTGTTCAAGGGCTCCCGATCGACGAGTTCTCAAGAAAGA					: 323	
LpMDHh61	:TTGCTCGGTGGTGAATGGACAATTGTTCAAGGGCTCCCGATCGACGAGTTCTCAAGAAAGA					: 318	
LpMDHh62	:TTGCTCGGTGGTGAATGGACAATTGTTCAAGGGCTCCCGATCGACGAGTTCTCAAGAAAGA	C	H	T	CCC	GAAAGCCGAGTTCTC-TTTAG-	: 28
LpMDHh63	:	-	-	-	-	-	-
LpMDHh64	:	-	-	-	-	-	-

	1060	*	1080	*	1100	*
LpMDHh1	:	-	-	-	-	-
LpMDHh2	:	-	-	-	-	-
LpMDHh3	:	-	-	-	-	-
LpMDHh4	:	-	-	-	-	-
LpMDHh5	:	-	-	-	-	-
LpMDHh6	:	-	-	-	-	-
LpMDHh7	:	-	-	-	-	-
LpMDHh8	:	-	-	-	-	-
LpMDHh9	:	-	-	-	-	-
LpMDHh10	:	-	-	-	-	-
LpMDHh11	:	-	-	-	-	-
LpMDHh12	:	-	-	-	-	-
LpMDHh13	:	-	-	-	-	-
LpMDHh14	:	-	-	-	-	-
LpMDHh15	:	-	-	-	-	-
LpMDHh16	:	-	-	-	-	-
LpMDHh17	:	-	-	-	-	-
LpMDHh18	:	-	-	-	-	-
LpMDHh19	:	-	-	-	-	-
LpMDHh20	:	-	-	-	-	-
LpMDHh21	:	-	-	-	-	-
LpMDHh22	:	-	-	-	-	-
LpMDHh23	:	-	-	-	-	-
LpMDHh24	:	-	-	-	-	-
LpMDHh25	:	-	-	-	-	-
LpMDHh26	:	-	-	-	-	-
LpMDHh27	:	-	-	-	-	-
LpMDHh28	:	-	-	-	-	-
LpMDHh29	:	-	-	-	-	-
LpMDHh30	:	-	-	-	-	-
LpMDHh31	:	-	-	-	-	-
LpMDHh32	:	-	-	-	-	-
LpMDHh34	:	-	-	-	-	-
LpMDHh35	:	-	-	-	-	-
LpMDHh36	:	-	-	-	-	-
LpMDHh37	:	-	-	-	-	-
LpMDHh38	:	-	-	-	-	-
LpMDHh39	:	-	-	-	-	-
LpMDHh40	:	-	-	-	-	-
LpMDHh41	:	-	-	-	-	-
LpMDHh42	:	-	-	-	-	-
) LpMDHh43	:	-	-	-	-	-
LpMDHh44	:	-	-	-	-	-
LpMDHh45	:	-	-	-	-	-
LpMDHh46	:	-	-	-	-	-
LpMDHh47	:	-	-	-	-	-
LpMDHh48	:	-	-	-	-	-
LpMDHh49	:	-	-	-	-	-
LpMDHh50	:	-	-	-	-	-
LpMDHh51	:	-	-	-	-	-
LpMDHh52	:	-	-	-	-	-
LpMDHh53	:	-	-	-	-	-
LpMDHh54	:	-	-	-	-	-
LpMDHh55	:	AGATGGATGCCACAGCCCAGGAGCTCGGAGGAGAAGGCTCTGCC	TA	CTCGGCTCGAG	:	-
LpMDHh56	:	AGATGGATGCCACAGCCCAGGAGCTCGGNAGGAGAAGGCTCTGCC	TA	CTCGGCTCGAG	:	660
LpMDHh57	:	AGATGGATGCCACAGCCCAGGAGCTCGGAGGAGAAGGCTCTGCC	TA	CTCGGCTCGAG	:	640
LpMDHh58	:	AGATGGATGCCACAGCCCAGGAGCTCGGAGGAGAAGGCTCTGCC	TA	CTCGGCTCGAG	:	636
LpMDHh59	:	AGATGGATGCCACAGCCCAGGAGCTCGGAGGAGAAGGCTCTGCC	TA	CTCGGCTCGAG	:	439
LpMDHh60	:	AGATGGATGCCACAGCCCAGGAGCTCGGAGGAGAAGGCTCTGCC	TA	CTCGGCTCGAG	:	421
LpMDHh61	:	AGATGGATGCCACAGCCCAGGAGCTCGGAGGAGAAGGCTCTGCC	TA	CTCGGCTCGAG	:	385
LpMDHh62	:	AGA-GGA <del>G</del> GCCACAGCCCAGGAGCTCGGAGGAGAAGGCTCTGCC	TA	CTCGGCTCGAG	:	380
LpMDHh63	:	-----@CTCGGAGGAGAAGGCTCTGCC	TA	CTCGGCTCGAG	:	89
LpMDHh64	:	-----	-----	-----	:	38

1120

\* 1140

\* 1160

\* 11

LpMDHh1	:					
LpMDHh2	:					
LpMDHh3	:					
LpMDHh4	:					
LpMDHh5	:					
LpMDHh6	:					
LpMDHh7	:					
LpMDHh8	:					
LpMDHh9	:					
LpMDHh10	:					
LpMDHh11	:					
LpMDHh12	:					
LpMDHh13	:					
LpMDHh14	:					
LpMDHh15	:					
LpMDHh16	:					
LpMDHh17	:					
LpMDHh18	:					
LpMDHh19	:					
LpMDHh20	:					
LpMDHh21	:					
LpMDHh22	:					
LpMDHh23	:					
LpMDHh24	:					
LpMDHh25	:					
LpMDHh26	:					
LpMDHh27	:					
LpMDHh28	:					
LpMDHh29	:					
LpMDHh30	:					
LpMDHh31	:					
LpMDHh32	:					
LpMDHh34	:					
LpMDHh35	:					
LpMDHh36	:					
LpMDHh37	:					
LpMDHh38	:					
LpMDHh39	:					
LpMDHh40	:					
LpMDHh41	:					
LpMDHh42	:					
LpMDHh43	:					
LpMDHh44	:					
LpMDHh45	:					
LpMDHh46	:					
LpMDHh47	:					
LpMDHh48	:					
LpMDHh49	:					
LpMDHh50	:					
LpMDHh51	:					
LpMDHh52	:					
LpMDHh53	:					
LpMDHh54	:					
LpMDHh55	:	TAACTGCATACCAAGGGAGCAGCTGCCGCTCTGATTTGAATAAAAGGAACATTTGGCTN				722
LpMDHh56	:	TAACTGCATACCAAGGGAGCAGCTGCCGCTCTGATTTGAATAAAAGGAACATTTGGCTN				701
LpMDHh57	:	TAACTGCATACCAAGGGAGCAGCTGCCGCTCTGATTTGAATAAAAGGAACATTTGGCTN				667
LpMDHh58	:	TAACTGCATACCAAGGGAGCAGCTGCCGCTCTGATTTGAATAAAAGGAACATTTGGCTC				501
LpMDHh59	:	TAACTGCATACCAAGGGAGCAGCTGCCGCTCTGATTTGAATAAAAGGAACATTTGGCTC				483
LpMDHh60	:	TAACTGCATACCAAGGGAGCAGCTGCCGCTCTGATTTGAATAAAAGGAACATTTGGCTC				447
LpMDHh61	:	TAACTGCATACCAAGGGAGCAGCTGCCGCTCTGATTTGAATAAAAGGAACATTTGGCTC				442
LpMDHh62	:	TAACTGCATACCAAGGGAGCAGCTGCCGCTCTGATTTGAATAAAAGGAACATTTGGCTC				151
LpMDHh63	:	TAACTGCATACCAAGGGAGCAGCTGCCGCTCTGATTTGAATAAAAGGAACATTTGGCTC				100
LpMDHh64	:					

	80	*	1200	*	1220	*	1240	
LpMDHh1	:	-	-	-	-	-	-	-
LpMDHh2	:	-	-	-	-	-	-	-
LpMDHh3	:	-	-	-	-	-	-	-
LpMDHh4	:	-	-	-	-	-	-	-
LpMDHh5	:	-	-	-	-	-	-	-
LpMDHh6	:	-	-	-	-	-	-	-
LpMDHh7	:	-	-	-	-	-	-	-
LpMDHh8	:	-	-	-	-	-	-	-
LpMDHh9	:	-	-	-	-	-	-	-
LpMDHh10	:	-	-	-	-	-	-	-
LpMDHh11	:	-	-	-	-	-	-	-
LpMDHh12	:	-	-	-	-	-	-	-
LpMDHh13	:	-	-	-	-	-	-	-
LpMDHh14	:	-	-	-	-	-	-	-
LpMDHh15	:	-	-	-	-	-	-	-
LpMDHh16	:	-	-	-	-	-	-	-
LpMDHh17	:	-	-	-	-	-	-	-
LpMDHh18	:	-	-	-	-	-	-	-
LpMDHh19	:	-	-	-	-	-	-	-
LpMDHh20	:	-	-	-	-	-	-	-
LpMDHh21	:	-	-	-	-	-	-	-
LpMDHh22	:	-	-	-	-	-	-	-
LpMDHh23	:	-	-	-	-	-	-	-
LpMDHh24	:	-	-	-	-	-	-	-
LpMDHh25	:	-	-	-	-	-	-	-
LpMDHh26	:	-	-	-	-	-	-	-
LpMDHh27	:	-	-	-	-	-	-	-
LpMDHh28	:	-	-	-	-	-	-	-
LpMDHh29	:	-	-	-	-	-	-	-
LpMDHh30	:	-	-	-	-	-	-	-
LpMDHh31	:	-	-	-	-	-	-	-
LpMDHh32	:	-	-	-	-	-	-	-
LpMDHh34	:	-	-	-	-	-	-	-
LpMDHh35	:	-	-	-	-	-	-	-
LpMDHh36	:	-	-	-	-	-	-	-
LpMDHh37	:	-	-	-	-	-	-	-
LpMDHh38	:	-	-	-	-	-	-	-
LpMDHh39	:	-	-	-	-	-	-	-
LpMDHh40	:	-	-	-	-	-	-	-
LpMDHh41	:	-	-	-	-	-	-	-
LpMDHh42	:	-	-	-	-	-	-	-
LpMDHh43	:	-	-	-	-	-	-	-
LpMDHh44	:	-	-	-	-	-	-	-
LpMDHh45	:	-	-	-	-	-	-	-
LpMDHh46	:	-	-	-	-	-	-	-
LpMDHh47	:	-	-	-	-	-	-	-
LpMDHh48	:	-	-	-	-	-	-	-
LpMDHh49	:	-	-	-	-	-	-	-
LpMDHh50	:	-	-	-	-	-	-	-
LpMDHh51	:	-	-	-	-	-	-	-
LpMDHh52	:	-	-	-	-	-	-	-
LpMDHh53	:	-	-	-	-	-	-	-
LpMDHh54	:	-	-	-	-	-	-	-
LpMDHh55	:	CATGAAACTCAT	-	-	-	-	-	734
LpMDHh56	:	CATG-	-	-	-	-	-	705
LpMDHh57	:	-	-	-	-	-	-	-
LpMDHh58	:	CATGAAACTCATCTCCACTCAGAACAGTTGCACATCGCGGTGCCTT	AGCTGGTTTCAG	-	-	-	-	563
LpMDHh59	:	CATGAAACTCATCTCCACTCAGAACAGTTGCACATCGCGGTGCCTT	AGCTGGTTTCAG	-	-	-	-	545
LpMDHh60	:	CATGAAACTCATCTCCACTCAGAACAGTTGCACATCGCGGTGCCTT	AGCTGGTTTCAG	-	-	-	-	509
LpMDHh61	:	CATGAAACTCATCTCCACTCAGAACAGTTGCACATCGCGGTGCCTT	AGCTGGTTTCAG	-	-	-	-	504
LpMDHh62	:	CATGAAACTCATCTCCACTCAGAACAGTTGCACATCGCGGTGCCTT	AGCTGGTTTCAG	-	-	-	-	213
LpMDHh63	:	CATGAAACTCATCTCCACTCAGAACAGTTGCACATCGCGGTGCCTT	AGCTGGTTTCAG	-	-	-	-	162
LpMDHh64	:	-	-	-	-	-	-	-

\* 1260 \* 1280 \* 1300

LpMDHh1	:	-	-	-
LpMDHh2	:	-	-	-
LpMDHh3	:	-	-	-
LpMDHh4	:	-	-	-
LpMDHh5	:	-	-	-
LpMDHh6	:	-	-	-
LpMDHh7	:	-	-	-
LpMDHh8	:	-	-	-
LpMDHh9	:	-	-	-
LpMDHh10	:	-	-	-
LpMDHh11	:	-	-	-
LpMDHh12	:	-	-	-
LpMDHh13	:	-	-	-
LpMDHh14	:	-	-	-
LpMDHh15	:	-	-	-
LpMDHh16	:	-	-	-
LpMDHh17	:	-	-	-
LpMDHh18	:	-	-	-
LpMDHh19	:	-	-	-
LpMDHh20	:	-	-	-
LpMDHh21	:	-	-	-
LpMDHh22	:	-	-	-
LpMDHh23	:	-	-	-
LpMDHh24	:	-	-	-
LpMDHh25	:	-	-	-
LpMDHh26	:	-	-	-
LpMDHh27	:	-	-	-
LpMDHh28	:	-	-	-
LpMDHh29	:	-	-	-
LpMDHh30	:	-	-	-
LpMDHh31	:	-	-	-
LpMDHh32	:	-	-	-
LpMDHh34	:	-	-	-
LpMDHh35	:	-	-	-
LpMDHh36	:	-	-	-
LpMDHh37	:	-	-	-
LpMDHh38	:	-	-	-
LpMDHh39	:	-	-	-
LpMDHh40	:	-	-	-
LpMDHh41	:	-	-	-
LpMDHh42	:	-	-	-
LpMDHh43	:	-	-	-
LpMDHh44	:	-	-	-
LpMDHh45	:	-	-	-
LpMDHh46	:	-	-	-
LpMDHh47	:	-	-	-
LpMDHh48	:	-	-	-
LpMDHh49	:	-	-	-
LpMDHh50	:	-	-	-
LpMDHh51	:	-	-	-
LpMDHh52	:	-	-	-
LpMDHh53	:	-	-	-
LpMDHh54	:	-	-	-
LpMDHh55	:	-	-	-
LpMDHh56	:	-	-	-
LpMDHh57	:	-	-	-
LpMDHh58	:	TGTGTATGAATGAGGCTTTGTAGCTCTATTTGCCTGATGATTACAGGGACAGGGATATTG	:	625
LpMDHh59	:	TGTGTATGAATGAGGCTTTGTAGCTCTATTTGCCTGATGATTACAGGGACAGGGATATTG	:	607
LpMDHh60	:	TGTGTATGAATGAGGCTTTGTAGCTCTATTTGCCTGATGATTACAGGGACAGGGATATTG	:	571
LpMDHh61	:	TGTGTATGAATGAGGCTTTGTAGCTCTATTTGCCTGATGATTACAGGGACAGGGATATTG	:	566
LpMDHh62	:	TGTGTATGAATGAGGCTTTGTAGCTCTATTTGCCTGATGATTACAGGGACAGGGATATTG	:	275
LpMDHh63	:	TGTGTATGAATGAGGCTTTGTAGCTCTATTTGCCTGATGATTACAGGGACAGGGATATTG	:	224
LpMDHh64	:	GNAKGNAGCTTTGTAGCTCTATTTGCCTGAGATTACAGGGACAGGGATATTG	:	55

\* 1320 \* 1340 \* 1360

LpMDHh1	:					
LpMDHh2	:					
LpMDHh3	:					
LpMDHh4	:					
LpMDHh5	:					
LpMDHh6	:					
LpMDHh7	:					
LpMDHh8	:					
LpMDHh9	:					
LpMDHh10	:					
LpMDHh11	:					
LpMDHh12	:					
LpMDHh13	:					
LpMDHh14	:					
LpMDHh15	:					
LpMDHh16	:					
LpMDHh17	:					
LpMDHh18	:					
LpMDHh19	:					
LpMDHh20	:					
LpMDHh21	:					
LpMDHh22	:					
LpMDHh23	:					
LpMDHh24	:					
LpMDHh25	:					
LpMDHh26	:					
LpMDHh27	:					
LpMDHh28	:					
LpMDHh29	:					
LpMDHh30	:					
LpMDHh31	:					
LpMDHh32	:					
LpMDHh34	:					
LpMDHh35	:					
LpMDHh36	:					
LpMDHh37	:					
LpMDHh38	:					
LpMDHh39	:					
LpMDHh40	:					
LpMDHh41	:					
LpMDHh42	:					
LpMDHh43	:					
LpMDHh44	:					
LpMDHh45	:					
LpMDHh46	:					
LpMDHh47	:					
LpMDHh48	:					
LpMDHh49	:					
LpMDHh50	:					
LpMDHh51	:					
LpMDHh52	:					
LpMDHh53	:					
LpMDHh54	:					
LpMDHh55	:					
LpMDHh56	:					
LpMDHh57	:					
LpMDHh58	:	GCAGGAAGATTGGAACAATTTGACGTCTGATTA A	AAA	CCAA	CCCTCTTATTATTCCCGTGTGTA	: 687
LpMDHh59	:	GCAGGAAGATTGGAACAATTTGACGTCTGATTA A	AAA	CCAA	CCCTCTTATTATTCCCTGTGTGTA	: 646
LpMDHh60	:	GCAGGAAGATTGGAACAATTTGACGTCTGATTA A	AAA	CCAA	CCCTCTTATTATTCCCTGTGTGTA	: 633
LpMDHh61	:	GCAGGAAGATTGGAACAATTTGACGTCTGATTA A	AAA	CCAA	CCCTCTTATTATTCCCTGTGTGTA	: 616
LpMDHh62	:	GCAGGAAGATTGGAACAATTTGACGTCTGATTA A	AAA	CCAA	CCCTCTTATTATTCCCTGTGTGTA	: 337
LpMDHh63	:	GCAGGAAGATTGGAACAATTTGACGTCTGATTA A	AAA	CCAA	CCCTCTTATTATTCCCTGTGTGTA	: 265
LpMDHh64	:	GCAGGAAGATTGGAACAATTTGACGTCTGATTA A	AAA	CCAA	CCCTCTTATTATTCCCTGTGTGTA	: 116

	*	1380	*	1400	*	1420	
LpMDHh1	:						
LpMDHh2	:						
LpMDHh3	:						
LpMDHh4	:						
LpMDHh5	:						
LpMDHh6	:						
LpMDHh7	:						
LpMDHh8	:						
LpMDHh9	:						
LpMDHh10	:						
LpMDHh11	:						
LpMDHh12	:						
LpMDHh13	:						
LpMDHh14	:						
LpMDHh15	:						
LpMDHh16	:						
LpMDHh17	:						
LpMDHh18	:						
LpMDHh19	:						
LpMDHh20	:						
LpMDHh21	:						
LpMDHh22	:						
LpMDHh23	:						
LpMDHh24	:						
LpMDHh25	:						
LpMDHh26	:						
LpMDHh27	:						
LpMDHh28	:						
LpMDHh29	:						
LpMDHh30	:						
LpMDHh31	:						
LpMDHh32	:						
LpMDHh34	:						
LpMDHh35	:						
LpMDHh36	:						
LpMDHh37	:						
LpMDHh38	:						
LpMDHh39	:						
LpMDHh40	:						
LpMDHh41	:						
LpMDHh42	:						
LpMDHh43	:						
LpMDHh44	:						
LpMDHh45	:						
LpMDHh46	:						
LpMDHh47	:						
LpMDHh48	:						
LpMDHh49	:						
LpMDHh50	:						
LpMDHh51	:						
LpMDHh52	:						
LpMDHh53	:						
LpMDHh54	:						
LpMDHh55	:						
LpMDHh56	:						
LpMDHh57	:						
LpMDHh58	:	TGAATGAGGCTTTGTAGCTCTATTTCGCCTGATGATTACAGGCCATGATATTGGCAGG					748
LpMDHh59	:						
LpMDHh60	:	TGAATGAGGCTTTGTAGCTCTATTTCGCCTGATGATTACAGGCCATGATATTGGCAGGA					695
LpMDHh61	:						
LpMDHh62	:	TGAATGAGGCTTTGTAGCTCTATTTCGCCTGATGATTACAGGCCATGATATTGGCAGGA					399
LpMDHh63	:						
LpMDHh64	:	TGAATGAGGCTTTGTAGCTCTATTTCGCCTGATGATTACAGGCCATGATATTGGCAGGA					178

	*	1440	*	1460	*	1480	
LpMDHh1	:	-	-	-	-	-	-
LpMDHh2	:	-	-	-	-	-	-
LpMDHh3	:	-	-	-	-	-	-
LpMDHh4	:	-	-	-	-	-	-
LpMDHh5	:	-	-	-	-	-	-
LpMDHh6	:	-	-	-	-	-	-
LpMDHh7	:	-	-	-	-	-	-
LpMDHh8	:	-	-	-	-	-	-
LpMDHh9	:	-	-	-	-	-	-
LpMDHh10	:	-	-	-	-	-	-
LpMDHh11	:	-	-	-	-	-	-
LpMDHh12	:	-	-	-	-	-	-
LpMDHh13	:	-	-	-	-	-	-
LpMDHh14	:	-	-	-	-	-	-
LpMDHh15	:	-	-	-	-	-	-
LpMDHh16	:	-	-	-	-	-	-
LpMDHh17	:	-	-	-	-	-	-
LpMDHh18	:	-	-	-	-	-	-
LpMDHh19	:	-	-	-	-	-	-
LpMDHh20	:	-	-	-	-	-	-
LpMDHh21	:	-	-	-	-	-	-
LpMDHh22	:	-	-	-	-	-	-
LpMDHh23	:	-	-	-	-	-	-
LpMDHh24	:	-	-	-	-	-	-
LpMDHh25	:	-	-	-	-	-	-
LpMDHh26	:	-	-	-	-	-	-
LpMDHh27	:	-	-	-	-	-	-
LpMDHh28	:	-	-	-	-	-	-
LpMDHh29	:	-	-	-	-	-	-
LpMDHh30	:	-	-	-	-	-	-
LpMDHh31	:	-	-	-	-	-	-
LpMDHh32	:	-	-	-	-	-	-
LpMDHh34	:	-	-	-	-	-	-
LpMDHh35	:	-	-	-	-	-	-
LpMDHh36	:	-	-	-	-	-	-
LpMDHh37	:	-	-	-	-	-	-
LpMDHh38	:	-	-	-	-	-	-
LpMDHh39	:	-	-	-	-	-	-
LpMDHh40	:	-	-	-	-	-	-
LpMDHh41	:	-	-	-	-	-	-
LpMDHh42	:	-	-	-	-	-	-
LpMDHh43	:	-	-	-	-	-	-
LpMDHh44	:	-	-	-	-	-	-
LpMDHh45	:	-	-	-	-	-	-
LpMDHh46	:	-	-	-	-	-	-
LpMDHh47	:	-	-	-	-	-	-
LpMDHh48	:	-	-	-	-	-	-
LpMDHh49	:	-	-	-	-	-	-
LpMDHh50	:	-	-	-	-	-	-
LpMDHh51	:	-	-	-	-	-	-
LpMDHh52	:	-	-	-	-	-	-
LpMDHh53	:	-	-	-	-	-	-
LpMDHh54	:	-	-	-	-	-	-
LpMDHh55	:	-	-	-	-	-	-
LpMDHh56	:	-	-	-	-	-	-
LpMDHh57	:	-	-	-	-	-	-
LpMDHh58	:	-	-	-	-	-	-
LpMDHh59	:	-	-	-	-	-	-
LpMDHh60	:	GGATTGGAACAATTCGACGCCTGATTA AAACCAACCTCTTATTACTA AAAAAAAAAAAA	-	-	-	750	-
LpMDHh61	:	-	-	-	-	-	-
LpMDHh62	:	GGATTGGAACAANN ANN	-	-	-	418	-
LpMDHh63	:	-	-	-	-	-	-
LpMDHh64	:	GGATTGGAACAATTCGACGC CTGATTA AAACCAACCTCTTATT A TTG G AAAAAAAAAAA	-	-	-	236	-

Figure 31 Nucleotide sequence of LpMDHi

\* 20 \* 40 \* 60  
LpMDHi : GTNCATAAAGCTGCCAAAGCAATNCGTGNAAATTATTCAGTAACCCTGTCAATTCTACC : 60

\* 80 \* 100 \* 120  
LpMDHi : GTACCAATTGCTGCTGAAGTATTAAAAAGCTGGGACATACAATNCTAAGAGATTGTTG : 120

\* 140 \* 160 \*  
LpMDHi : GGGGTTGACAACNGTTNGATGNNANTGACAGACCNTGCTCTNGNNNGCAGGTCNC : 177

Figure 32 Deduced amino acid sequence of LpMDHi

\* 20 \* 40 \*  
LpMDHi : XHKAAQSNXXNIISNPVNSTVPIAAEVFKKAGTYNXKRLLGVDNXXMXXTDXALXXRG : 58

Figure 33 Nucleotide sequence of LpMDHj

\* 20 \* 40 \* 60  
LpMDHj : ANAAAGGAGCCGACGCAGGGCGCAGAATTCCATCTGCTNACTCTGCCACCACCCAAGTT : 60

\* 80 \* 100 \* 120  
LpMDHj : GGACATGGCGTCAGCTGTTACAATCAGTCAGTCAGCGCGCAGGCCGCTTGGTTCAAA : 120

\* 140 \* 160 \* 180  
LpMDHj : ACCAAGGAACCATGGCAGCACGAGCTACAGTGGCTAAAGGCATCATCGTCGTCGATCAG : 180

\* 200 \* 220 \* 240  
LpMDHj : CTTCGAACATCAGGAACATCATT CCTGGCAAGACCGCCTCCCTCCGGCAACTGTTACAC : 240

\* 260 \* 280 \* 300  
LpMDHj : AAGGGTTGTGCCAAAGGCAGAGTCTGGGTCGCAGATATCGCCTCAGGCATCTTACAAGGT : 300

\* 320 \* 340 \* 360  
LpMDHj : GGCGGTGCTTGGTGCTGCTGGTGGCATCGTCACCACGTGGCCTGCTGATCAAGATGTC : 360

\* 380 \* 400 \* 420  
LpMDHj : TCCTCTGGTCTCGGAGCTGCGCCTGTATGATATCGCAATGTCAAGGGCGTCGCTGCAGA : 420

\* 440 \* 460 \* 480  
LpMDHj : TCTCAGCCACTGCAACACCGCCTGCTCAGGT CATGGACTTC ACTGGCCCCGAGAGCTAGC : 480

\* 500 \* 520 \* 540  
LpMDHj : AGAGTGCTTGAAAGGTGTGGATGTTGTCGTCATCCCTGCGGGTGTCCAAGGAAGGCCAGG : 540

\* 560 \* 580 \* 600  
LpMDHj : CATGACCCGTGATGACCTTTAACATNAATGCGGAATCGNCAAGTCGTTATTGAGGC : 600

\* 620 \* 640 \* 660  
LpMDHj : TGTTGCAGACAATTGCCCTGAGGGCTTATTCAATCATCAACAACCCGGTCAAACCTCC : 660

LpMDHj : CCCT : 664

Figure 34 Deduced amino acid sequence of LpMDHj

\* 20 \* 40 \* 60  
LpMDHj : XRSRRRGAEFHLXTLPPP KLDMASAVTISSVSAQAA LVSKPRNHGSTSYSGLKASSSSIS : 60

\* 80 \* 100 \* 120  
LpMDHj : FESGTSFLGKTASLRATVTTRVVPKAKSGSQISPQASYKVALGAAGGGIGQPLGLLIKMS : 120

\* 140 \* 160 \* 180  
LpMDHj : PLVSELRLYDIAVKGVAADLSHCNTPAQVMDFTGPAELAECLKGVVVVIPAGVPRKPG : 180

\* 200 \* 220  
LpMDHj : MTRDDLFNXNAGIXXSLIEAVADNCPEGLIHIINNPGQTTPP : 221

Figure 35 Consensus contig nucleotide sequence of LpMDHk

LpMDHk :	* 20 * 40 * 60	
	TNTTANCCNCCAANTATCCAGNANCACCTGGCCCTACACANAANAAAACAAAAANN	: 60
LpMDHk :	* 80 * 100 * 120	
	AACCAGNACGCAAGGGGCGAGCCGGGCGCACGCAGCAATTCCCATCTGCTCACCAACCC	: 120
LpMDHk :	* 140 * 160 * 180	
	AAGTTGGAGATGGCATCAGCTGTACCATCAGCTCAGTCAGCGCGCAGGCCGTTGGTC	: 180
LpMDHk :	* 200 * 220 * 240	
	TCGAAACCAAGGAATCATGGCAGCACAGCTACAGTGGCTAAAGGCATCATCGTCG	: 240
LpMDHk :	* 260 * 280 * 300	
	ATCAGCTTCGAATCAGGGACATCATT CCTGGCAAGACC GGCTCTCTCGGGCGACTATC	: 300
LpMDHk :	* 320 * 340 * 360	
	ACCTCAAGGATTGCCAAGGC AAGTCTGGTCTCAGATATCACCTCAGGCCCTCGTAC	: 360
LpMDHk :	* 380 * 400 * 420	
	AAGGTGGCGGTGCTTGGTGCTGCCGGTGGCATCGGTCAACC ACTGGCCTGCTGATCAAG	: 420
LpMDHk :	* 440 * 460 * 480	
	ATGTCTCCTCTGGTCTCAGAGCTGCGCCTGTATGATATTGCCAATGTC AAGGGAGTCGCT	: 480
LpMDHk :	* 500 * 520 * 540	
	GCAGATCTCAGCCACTGCAACACAGCCTCTCAGGTCA TGGACTTC ACTGGCCCAGCAGAA	: 540
LpMDHk :	* 560 * 580 * 600	
	CTAGCTGACTGCTTGAAAGGTGTTGATGTTGTCGTCATCCCTGCGGGTGTCCCAGGAAG	: 600
LpMDHk :	* 620 * 640 * 660	
	CCAGGCATGACCCGTGATGACCTTTAACATCAATGCGGGCATCGTCAAGTCGCTTATT	: 660
LpMDHk :	* 680 * 700 * 720	
	GAGGCTGTTGCAGACA ACTGCCCTGAGGCCTTCATCCATATCATCAGCAACCCGGTCAAC	: 720
LpMDHk :	* 740 * 760 * 780	
	TCCACTGTGCCGATTGCTGCTGAGATTCTGAAACAGAAGGGCGTCTACAACCCCAAGAAG	: 780
LpMDHk :	* 800 * 820 * 840	
	CTCTTCGGGGTTCCACCCCTGGATGTTGTCAGAGCTAACACATTGTAGCTCAGAAGAAG	: 840
LpMDHk :	* 860 * 880 * 900	
	AACCTCAGCCTCATCGATGTTGATGTCCCAGTTGTCGGTGGCCATGCTGGGATCAGGATT	: 900
LpMDHk :	* 920 * 940 * 960	
	CTGCCTCTGTTGCCAAGACTAGGCCTTCTGTCAGCTTCACGGACGAGGAACTGAACAG	: 960

\* 980 \* 1000 \* 1020  
LpMDHk : CTGACAAAGAGGATACAGAACGCTGGACAGAGGCAGGGTGGAGGCGAAGGCTGGTGTGGC : 1020

\* 1040 \* 1060 \* 1080  
LpMDHk : TCTGCTACTCTGCCATGGCTTATGCCGCTGCCAGATTGTTGAGTCATCGCTCCCGCA : 1080

\* 1100 \* 1120 \* 1140  
LpMDHk : ATGGCTGGTGATCCAGATGTTACGAGTGCACGTATGTTCACTGAGTTAACAGAGCTT : 1140

\* 1160 \* 1180 \* 1200  
LpMDHk : CCATTCTCGCGTCCAGAGTTAACGCTGGGAAGGACGGNGTTGAGTCATCATTCCCTCC : 1200

\* 1220 \* 1240 \* 1260  
LpMDHk : GACCTGGAGGGAGTGACGGAGTACGAGGCCAAGGCGCTTGANGCATTGAAGGCTGAGCTG : 1260

LpMDHk : AAG : 1263

Figure 36 Deducing amino acid sequence of LpMDHk

\* 20 \* 40 \* 60  
LpMDHk : XLXXQXSXXHLALHXXKTKXNQXARGEPGRTQQFPSAHQPKLEMASAVTISSVSAQAALV : 60

\* 80 \* 100 \* 120  
LpMDHk : SKPRNHGSTSYSGLKASSSSISFESGTSFLGKTASLRATITSRIVPKAKSGSQISPQASY : 120

\* 140 \* 160 \* 180  
LpMDHk : KVALGAAGGIGQPLGLLIKMSPLVSELRLYDIANVKVAAADLSHCNTPSQVMDFGTGPAB : 180

\* 200 \* 220 \* 240  
LpMDHk : LADCLKGVDVVVIPAGVPRKPGMTRDDLFNINAGIVKSLIEAVADNCPEAFIHIISNPVN : 240

\* 260 \* 280 \* 300  
LpMDHk : STVPIAAEILKQKGVYNPKKLFGVSTLDVVRANTFVAQKKNLSSLIDVDVPVVGGHAGITI : 300

\* 320 \* 340 \* 360  
LpMDHk : LPULLSKTRPSVSFTDEETEQLTKRIQNAGTEAVEAKAGAGSATLSMAYAAARFVESSLRA : 360

\* 380 \* 400 \* 420  
LpMDHk : MAGDPDVYECTYVQSELTELPFFASRVKLGKDXVESIISSDLEGVTEYEAKALXALKEL : 420

LpMDHk : K : 421

Figure 37 Nucleotide sequences of nucleic acid fragments contributing to the consensus contig sequence LpMDHk

	*	20	*	40	*	60	
LpMDHk1	:	TNTTTANCCNCCAANTATCCAGNANCACCTG	GCCCCGAA	CCA	-AN	AAAAA	AAAAGN
LpMDHk2	:	-	-	GNGCCGG	CAC	CGA	AAAANN
LpMDHk3	:	-	-	GNCCCG	-C	AN	AAAAGC
LpMDHk4	:	-	-	GNCCCG	GC	AN	AAAANN
LpMDHk5	:	-	-	GCCCG	G	AN	AAAANN
LpMDHk6	:	-	-	GCON	-CA	NC	AAAAGC
LpMDHk7	:	-	-	GTC	TC	CA	AN
LpMDHk8	:	-	-	GTC	TC	CA	AN
LpMDHk9	:	-	-	GNN	AC	AC	AN
LpMDHk10	:	-	-	GTT	AC	AC	AN
LpMDHk11	:	-	-	CCT	-CA	AC	AA
LpMDHk12	:	-	-	TTC	CC	AN	AA
LpMDHk13	:	-	-	TCCC	CA	AN	AA
LpMDHk14	:	-	-	ACAC	AN	AA	AAAANN
LpMDHk15	:	-	-	ACAC	AN	AA	AAAANN
LpMDHk16	:	-	-	ACAC	AN	AA	AAAAG
LpMDHk17	:	-	-	CANN	NA	AA	AA
LpMDHk18	:	-	-	STT	CC	AA	AA
LpMDHk19	:	-	-	GNAC	G	AA	AA
LpMDHk20	:	-	-	GNAC	G	AA	AA
LpMDHk21	:	-	-	GNAC	G	AA	AA
LpMDHk22	:	-	-	GNAC	G	AA	AA
LpMDHk23	:	-	-	CAN	AN	AA	AA
LpMDHk24	:	-	-	CAN	AN	AA	AA
LpMDHk25	:	-	-	CANT	AN	AA	AA
LpMDHk26	:	-	-	CAN	AN	AA	AA
LpMDHk27	:	-	-	GAGC	G	AA	AA
LpMDHk28	:	-	-	GAGC	G	AA	AA
LpMDHk29	:	-	-	GAGC	G	AA	AA
LpMDHk30	:	-	-	AN	NA	AA	AA
LpMDHk31	:	-	-	AN	NA	AA	AA
LpMDHk32	:	-	-	AN	NA	AA	AA
LpMDHk33	:	-	-	AN	NA	AA	AA
LpMDHk34	:	-	-	NAG	AA	AA	AA
LpMDHk35	:	-	-	CAG	AA	AA	AA
LpMDHk36	:	-	-	AN	AA	AA	AA
LpMDHk37	:	-	-	NAAG	NN	AA	-
LpMDHk38	:	-	-	GNAC	AC	AN	NN
LpMDHk39	:	-	-	AA	AC	AA	AA
LpMDHk40	:	-	-	GNAC	AC	AN	NN
LpMDHk41	:	-	-	GA	NC	CA	NN
LpMDHk42	:	-	-	GA	TC	AA	NN
LpMDHk43	:	-	-	AA	AA	AA	AA
LpMDHk44	:	-	-	AAN	CO	AA	AA
LpMDHk45	:	-	-	AA	AC	AA	AA
LpMDHk46	:	-	-	GACA	AN	AA	NN
LpMDHk47	:	-	-	AA	AN	AA	AA
LpMDHk48	:	-	-	GN	-NN	AA	NN
LpMDHk49	:	-	-	C	-AN	AA	NN
LpMDHk50	:	-	-	GN	AC	GA	AA
LpMDHk51	:	-	-	GA	NN	NN	NN
LpMDHk52	:	-	-	GA	NN	NN	NN
LpMDHk53	:	-	-	GA	CC	AA	AA
LpMDHk54	:	-	-	GA	CC	AA	AA
LpMDHk55	:	-	-	AN	NN	NN	NN
LpMDHk56	:	-	-	GA	NN	NN	NN
LpMDHk57	:	-	-	GA	NN	NN	NN
LpMDHk58	:	-	-	GA	NN	NN	NN
LpMDHk59	:	-	-	GA	NN	NN	NN
LpMDHk60	:	-	-	GA	NN	NN	NN
LpMDHk61	:	-	-	GA	NN	NN	NN
LpMDHk62	:	-	-	GA	NN	NN	NN
LpMDHk63	:	-	-	GA	NN	NN	NN
LpMDHk64	:	-	-	GA	NN	NN	NN
LpMDHk65	:	-	-	GA	NN	NN	NN
LpMDHk66	:	-	-	GA	NN	NN	NN

	80	100	120	
LpMDHk1	: AGCCAGNACGCAAGGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCTCACCAACCC		: 118	
LpMDHk2	: A-CCAGNA-GC-AGGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCTCACCAACCC		: 85	
LpMDHk3	: AGCCAGNNCGCAAGGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCTCACCAACCC		: 86	
LpMDHk4	: A-CCAGNA-GC-AGGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCTCACCAACCC		: 84	
LpMDHk5	: ANCCAGNA-GC-AGGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCTCACCAACCC		: 85	
LpMDHk6	: AGCCAGNNCGCAAGGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCTCACCAACCC		: 84	
LpMDHk7	: ATCCAGNA-GC-AGGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCTCACCAACCC		: 82	
LpMDHk8	: NACCAGNACGC-AGGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCTCACCAACCC		: 83	
LpMDHk9	: A-CCAGNA-GCAAGGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCTCACCAACCC		: 83	
LpMDHk10	: A-CCAGNA-GC-AGGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCTCACCAACCC		: 82	
LpMDHk11	: AGC-TAGNCGCAAGGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCTCACCAACCC		: 81	
LpMDHk12	: NACCAGNN-GC-AGGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCTCACCAACCC		: 82	
LpMDHk13	: NACCAGNA-GC-AGNGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCTCACCAACCC		: 81	
LpMDHk14	: ACCA-TAG-GC-AGGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCTCACCAACCC		: 80	
LpMDHk15	: A-CCAGNA-GC-AGGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCTCACCAACCC		: 79	
LpMDHk16	: NACCAGNA-GCAAGGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCTCACCAACCC		: 79	
LpMDHk17	: NACCAGNN-GCAAGGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCTCACCAACCC		: 78	
LpMDHk18	: AGCCAG-NCGCAAGGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCTCACCAACCC		: 80	
LpMDHk19	: AGCCAGNACGCAAGGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCTCACCAACCC		: 80	
LpMDHk20	: AGCCAGNNCGCAAGGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCTCACCAACCC		: 80	
LpMDHk21	: AGCCAGNNCGCAAGGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCTCACCAACCC		: 80	
LpMDHk22	: AGCCAGNNCGCAAGGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCTCACCAACCC		: 80	
LpMDHk23	: A-CCAGNN-GC-AGGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCTCACCAACCC		: 77	
LpMDHk24	: A-CCAGNN-GC-AGGGGGCGACCCGGGGCGCACGCAGCAATTCCCATCTGCTCACCAACCC		: 77	
LpMDHk25	: A-CCAGNA-GCAAGGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCTCACCAACCC		: 77	
LpMDHk26	: ANCCAGNACGCAAGGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCTCACCAACCC		: 79	
LpMDHk27	: AGCCAG-NCGCAAGGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCTCACCAACCC		: 78	
LpMDHk28	: AGCCAGNNCGCAAGGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCTCACCAACCC		: 79	
LpMDHk29	: NCCAGNN-GCAAGGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCTCACCAACCC		: 74	
LpMDHk30	: NACCAGNACGCAAGGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCTCACCAACCC		: 78	
LpMDHk31	: A-CCAGNACGCAAGGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCTCACCAACCC		: 76	
LpMDHk32	: ANCCAGNA-GCAAGGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCTCACCAACCC		: 75	
LpMDHk33	: A-CCAGNACGCAAGGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCTCACCAACCC		: 75	
LpMDHk34	: AGCCAGA-GCAAGGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCTCACCAACCC		: 75	
LpMDHk35	: AGCCAG-AAGGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCTCACCAACCC		: 74	
LpMDHk36	: A-CCAGNACGCAAGGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCTCACCAACCC		: 74	
LpMDHk37	: A---A-GAAAAAAAGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCCAACCAACCC		: 67	
LpMDHk38	: AAAAAN-GAAAAGGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCCAACCAACCC		: 70	
LpMDHk39	: AGCCAGNA-GCAAGGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCTCACCAACCC		: 72	
LpMDHk40	: AAAAAN-GAAAAGGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCCAACCAACCC		: 69	
LpMDHk41	: AAAAANAAAAGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCCAACCAACCC		: 70	
LpMDHk42	: A---N-GAAAAGGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCCAACCAACCC		: 66	
LpMDHk43	: AGCCAG-NNGCAAGGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCTCACCAACCC		: 70	
LpMDHk44	: NACCAGNACGCA-GGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCTCACCAACCC		: 71	
LpMDHk45	: A-CCAGNACGCAAGGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCTCACCAACCC		: 70	
LpMDHk46	: AAAAAN-NAAAAGGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCCAACCAACCC		: 68	
LpMDHk47	: NACCAGNACGCA-GGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCTCACCAACCC		: 70	
LpMDHk48	: AAAAAN-NAAAAGGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCCAACCAACCC		: 66	
LpMDHk49	: AAAAAN-GAAAAGGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCCAACCAACCC		: 65	
LpMDHk50	: AAAAAGAAA-WAAAAGGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCCAACCAACCC		: 67	
LpMDHk51	: AAAAAN-GAAAAGGGNA-CGAGCCGGGGCGCACGCAGCAATTCCCATCTGCCAACCAACCC		: 66	
LpMDHk52	: AAAAANAAAAGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCCAACCAACCC		: 65	
LpMDHk53	: AAAAAGAAA-WAAAAGGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCCAACCAACCC		: 66	
LpMDHk54	: AAAAANAAA-WAAAAGGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCCAACCAACCC		: 64	
LpMDHk55	: AAAAAGAAA-WAAAAGGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCCAACCAACCC		: 63	
LpMDHk56	: -AAA-WAAAAGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCCAACCAACCC		: 57	
LpMDHk57	: -AAA-WAAAAGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCCAACCAACCC		: 57	
LpMDHk58	: -CAAGGGGGCGAGCCGGGGCGCACGCAGCAATTCCCATCTGCTCACCAACCC		: 50	
LpMDHk59	: -ANAGGGGCN-NCGGGGCGC-CGC-G-AATT-CCATCTGCTCACCAACCC		: 43	
LpMDHk60	: -GGAGCCGGGGCNC-CGCAGCAATTCCCATCTGCTCACCAACCC		: 42	
LpMDHk61	: -GGGGGCCACGC-CAATTCCCATCTGCTCACCAACCC		: 37	
LpMDHk62	: -NCA-GCAGCAATTCCCATCTGCTCACCAACCC		: 31	
LpMDHk63	: -GNCA-CNAAT-CCC-NCTGCCAACCAACCC		: 31	
LpMDHk64	: -TCTGCCAACCAACCC		: 15	
LpMDHk65	: -		-	
LpMDHk66	: -		-	

140

160

180



260

280

300

320

340

360

380

400

420









	680	700	720
LpMDHk1	GAGGCTGTTGCAGACAAC	CCCTGAGGCCCTTCATCCATATCATCANCNACCG	711
LpMDHk2	GAGGCTGTTGCAGACAAC	GTGAGGCCCTTCATCCATATCATCAGCAACCCGGTCAAC	647
LpMDHk3	GAGGCTGTTGCAGACAAC	GTGAGGCCCTTCATCCATATCATCAGCAACCCGGTCAAC	686
LpMDHk4	GAGGCTGTTGCAGACAAC	GTGAGGCCCTTCATCCATATCATCAGCAACCCGGTCAAC	684
LpMDHk5	GAGGCTGTTGCAGACAAC	GTGAGGCCCTTCATCCATATCATCAGCAACCCGGTCAAC	685
LpMDHk6	-	-	-
LpMDHk7	-	-	-
LpMDHk8	GAGGCTGTTGCAGACAAC	GTGAGGCCCTTCATCCATATCATCAGCAACCCGGTCAAC	659
LpMDHk9	GAGGCTGTTGCAGACAAC	GTGAGGCCCTTCATCCATATCATCAGCAACCCGGTCAAC	683
LpMDHk10	GAGGCTGTTGCAGACAAC	GTGAGGCCCTTCATCCATATCATCAGCAACCCGGTCAAC	682
LpMDHk11	GAGGCTGTTGCAGACAAC	GTGAGGCCCTTCATCCATATCATCAGCAACCCGGTCAAC	681
LpMDHk12	GAGGCTGTTGCAGACAAC	GTGAGGCCCTTCATCCATATCATCAGCAACCCGGTCAAC	682
LpMDHk13	GAGGCTGNTGCAGACAAC	GTGAGGCCCTTCATCCATATCATCAGCAACCCGGTCAAC	681
LpMDHk14	GAGGCTGTTGCAGACAAC	GTGAGGCCCTTCATCCATATCATCAGCAACCCGGTCAAC	680
LpMDHk15	GAGGCTGTTGCAGACAAC	GTGAGGCCCTTCATCCATATCATCAGCAACCCGGTCAAC	679
LpMDHk16	GAGGCTGNTGCAGACAAC	GTGAGGCCCTTCATCCATATCATCAGCAACCCGGTCAAC	679
LpMDHk17	GAGGCTGTTGCAGACAAC	GTGAGGCCCTTCATCCATATCATCAGCAACCCGGTCAAC	679
LpMDHk18	GAGGCTGTTGCAGACAAC	GTGAGGCCCTTCATCCATATCATCAGCAACCCGGTCAAC	679
LpMDHk19	GAGGCTGNTGCAGACAAC	GTGAGGCCCTTCATCCATATCATCAGCAACCCGGTCAAC	680
LpMDHk20	GAGGCTGTTGCAGACAAC	GTGAGGCCCTTCATCCATATCATCAGCAACCCGGTCAAC	680
LpMDHk21	GAGGCTGTTGCAGACAAC	GTGAGGCCCTTCATCCATATCATCAGCAACCCGGTCAAC	680
LpMDHk22	GAGGCTGTTGCAGACAAC	GTGAGGCCCTTCATCCATATCATCAGCAACCCGGTCAAC	680
LpMDHk23	GAGGCTGTTGC	-	-
LpMDHk24	GAGGCTGTTGCAGACAAC	GTGCC	628
LpMDHk25	GAGGCTGTTGCAGACAAC	GTGCC	640
LpMDHk26	GAGGCTGNTGCAGACAAC	GTGCC	677
LpMDHk27	GAGGCTGTTGCAGACAAC	GTGCC	679
LpMDHk28	GAGGCTGTTGCAGACAAC	GTGCC	678
LpMDHk29	GAGGCTGTTGCAGACAAC	GTGCC	679
LpMDHk30	GAGGCTGTTGCAGACAAC	GTGCC	674
LpMDHk31	GAGGCTGNTGCAGACAAC	GTGCC	678
LpMDHk32	GAGGCTGTTGCAGACAAC	GTGCC	676
LpMDHk33	GAGGCTGNTGCAGACAAC	GTGCC	637
LpMDHk34	GAGGCTGTTGCAGACAAC	GTGCC	675
LpMDHk35	GAGGCTGTTGCAGACAAC	GTGCC	675
LpMDHk36	GAGGCTGTTGCAGACAAC	GTGCC	674
LpMDHk37	GAGGCTGTTGCAGAC	ACT	674
LpMDHk38	GAGGCTGTTGCAGACAAC	GTGCC	659
LpMDHk39	GAGGCTGNTGCAGACAAC	GTGCC	669
LpMDHk40	GAGGCTGTTGCAGACAAC	GTGCC	644
LpMDHk41	GAGGCTGTTGCAGACAAC	GTGCC	669
LpMDHk42	GAGGCTGTTGCAGACAAC	GTGCC	670
LpMDHk43	CGATTGCTGAGACAACT	NACAGAA	666
LpMDHk44	GAGGCTGTTGCAGACAAC	GTGCC	637
LpMDHk45	GAGGCTGTTGCAGACAAC	GTGCC	671
LpMDHk46	GAGGCTGTTGCAGACAAC	GTGCC	670
LpMDHk47	GAGGCTGTTGCAGACAAC	GTGCC	647
LpMDHk48	GAGGCTGTTGCAGACAAC	GTGCC	661
LpMDHk49	GAGGCTGTTGCAGACAAC	GTGCC	640
LpMDHk50	GAGGCTGTTGCAGACAAC	GTGCC	665
LpMDHk51	GAGGCTGNTGCAGACAAC	GTGCC	667
LpMDHk52	GAGGCTGTTGCAGACAAC	GTGCC	665
LpMDHk53	GAGGCTGTTGCAGACAAC	GTGCC	665
LpMDHk54	GAGGCTGTTGCAGACAAC	GTGCC	666
LpMDHk55	GAGGCTGTTGCAGACAAC	GTGCC	664
LpMDHk56	GAGGCTGTTGCAGACAAC	GTGCC	663
LpMDHk57	GAGGCTGNTGCAGACAAC	GTGCC	657
LpMDHk58	-	-	-
LpMDHk59	GAGGCTGTTGCAGACAAC	GTGCC	-
LpMDHk60	GAGGCTGTTGCAGACAAC	GTGCC	639
LpMDHk61	GAGGCTGTTGCAGACAAC	GTGCC	642
LpMDHk62	-	-	-
LpMDHk63	GAGGCTGTTGCAGACAAC	GTGCC	635
LpMDHk64	GAGGCTGTTGCAGACAAC	GTGCC	629
LpMDHk65	GAGGCTGTTGCAGACAAC	GTGCC	615
LpMDHk66	GAGGCTGTTGCAGACAAC	GTGCC	347

	* 740 *	760	* 780
LpMDHk1	:	-	-
LpMDHk2	:	-	-
LpMDHk3	: TCCACGGTGCCGATTGCTGCTGAGATTCTGAAACAGAAGGGCGTCTACAACCCAAGAAG	: 746	
LpMDHk4	: TNCACTGT-----		: 692
LpMDHk5	: TNCACTGTGA-----		: 695
LpMDHk6	:	-	-
LpMDHk7	:	-	-
LpMDHk8	:	-	-
LpMDHk9	: TNCACTGTGCCGATTGCTGCTGA-----		: 706
LpMDHk10	: TCCACTGTGCCGATTGCTGCTGA-----		: 706
LpMDHk11	: TCCACGGTGCCGATTGCTGCTGAGATTCTGAAACAGAAGGGCGTNTACAACCCAAGAAG		: 741
LpMDHk12	: TNCACTGTG-----		: 691
LpMDHk13	: TNCACTGTGCCGATTGCTGCTGAG-----		: 705
LpMDHk14	:	-	-
LpMDHk15	: TCCACTGTGCCGATTGCTGCTGAGAT-----		: 705
LpMDHk16	: TNCACTGTGCCGATTGCTGCTGAGATA-----		: 706
LpMDHk17	:	-	-
LpMDHk18	: TCCACTGTGCCGATTGCTGCTGAGATTCTGAAACAGAAGGGCGTCTACAACCCAAGAAG		: 740
LpMDHk19	: TCCACTGTGCCGATTGCTGCTGAATTCTGAAACAGAAGGGCGNTACAACCCAAGAAG		: 740
LpMDHk20	: TCCACTGTGCCGATTGCTGCTGAGATTCTGAAACAGAAGGGCGTCTACAACCCAAGAAG		: 740
LpMDHk21	: TCCACTGTGCCGATTGCTGCTGAGATTCTGAAACAGAAGGGCGTCTACAACCCAAGAAG		: 740
LpMDHk22	: TCCACTGTGCCGATTGCTGCTGAGATTCTGAAACAGAAGGGCGTCTACAACCCAAGAAG		: 740
LpMDHk23	:	-	-
LpMDHk24	:	-	-
LpMDHk25	: TCCACTGTGCCGATTGCTGCT-----		: 698
LpMDHk26	: TNCACTGTGCCGATTGCTGCTGAGATTCTGAAAN-----		: 713
LpMDHk27	: TCCACTGTGCCGATTGCTGCTGAGATTCTGAAACAGAAGGGCGTCTACAACCCAAGAAG		: 738
LpMDHk28	: TCCACTGTGCCGATTGCTGCTGAGATTCTGAAACAGAAGGGCGTCTACAACCCAAGAAG		: 739
LpMDHk29	: TNCACTGTG-----		: 684
LpMDHk30	: TNCACTGTGCCGATTG-----		: 695
LpMDHk31	: TNCACTGTGCCGATTGCTG-----		: 695
LpMDHk32	:	-	-
LpMDHk33	:	-	-
LpMDHk34	: TCCACTGTGCCGATTGCTGCTGAGATTCTGAAACAGAAAGGC-----CTACAACCCAAGAAG		: 734
LpMDHk35	: TCCACGGTGCCGATTGCTGCTGAGATTCTGAAACAGAAGGGCGTCTACAACCCAAGAAG		: 734
LpMDHk36	: TNCACTGTGCCGATTGCTGCTGAGATTCTGAA-----		: 706
LpMDHk37	: TGCACGGTGCCGATTGCTGNAAT-----		: 682
LpMDHk38	: TCCACGGTGCCGATTGCTGAGAGATTCTGAAACAGAAAGGC-----		: 712
LpMDHk39	:	-	-
LpMDHk40	: TNCACGGTGCCGAT-----		
LpMDHk41	: TCCACGGTGCCGATTGCTGCAAGAGA-----		: 683
LpMDHk42	: TCCACGGTGCCGATTGCTGCTGAGATTCTGAAACAGAAGGGCGTCTACAACCCAAGAAG		: 695
LpMDHk43	:	-	-
LpMDHk44	: TNCACTGTGCCGATT-----		
LpMDHk45	: TNCACTGTGCCGATTGCTGCTG-----		: 686
LpMDHk46	:	-	-
LpMDHk47	:	-	-
LpMDHk48	:	-	-
LpMDHk49	: TCCACGGTGCCGATTG-----		
LpMDHk50	: TCCACGGTGCCGATTGCTGCAAGAGATTCTGAAACAGAAGGGCGTCTACAACCCAAGAAG		: 681
LpMDHk51	:	-	-
LpMDHk52	: TNCACGGTGCCGAT-----		
LpMDHk53	: TCCACGGTGCCGATTGCTGCAAGAGATTCTGAAACAGAAGGGCGTCTACAACCCAAGAAG		: 680
LpMDHk54	: TCCACGGTGCCGATTGCTGCAAGAGATTCTGAAACAGAAG-----		: 726
LpMDHk55	: TCCACGGTGCCGATTGCTGCAAGAGATTCTGAAACAGAAGGGCGTCTACAACCCAAGAAG		: 702
LpMDHk56	: TNCACGGTGCCGATTGCTGCAAGAGATTCTGAAACAAGAGCGTCTACAACAC-----		: 723
LpMDHk57	: TCCACGGTGCCGATTGCTGCAAGAGATTCTGAAACAGAAGGGCGTCTACAACAC-----		: 707
LpMDHk58	:	-	-
LpMDHk59	: TNC-----		
LpMDHk60	: TCCACTGTGCCGATTGCTGCTGAGATTCTGAAACAGAAGGGCGTCTACAACCCAAGAAG		: 642
LpMDHk61	: TNCACTGTGCCGATTGCTGCTGAGATTCTGAAACAGAAGGGCGTCTACAACAC-----		: 702
LpMDHk62	:	-	-
LpMDHk63	: T-----		
LpMDHk64	: TNCACGGTGCCGATTGCTGCAAGAGATTCTGAAACAGAAGGGCGTCTACAACAC-----		: 630
LpMDHk65	: TCCACTGTGCCGATTGCTGCTGAGATTCTGAAACAGAAGGGCGTCTACAACAC-----		: 671
LpMDHk66	: TCCACTGTGCCGATTGCTGCTGAGATTCTGAAACAGAAGGGCGTCTACAACAC-----		: 407
			: 294

	* 800	* 820	* 840	
LpMDHk1 :	-----			:
LpMDHk2 :	-----			:
LpMDHk3 :	CTCTTCGGGGTTTNCACCCCTGGATGTTGTCAGAGCTAACACACATTGTAGCTCA			: 801
LpMDHk4 :	-----			:
LpMDHk5 :	-----			:
LpMDHk6 :	-----			:
LpMDHk7 :	-----			:
LpMDHk8 :	-----			:
LpMDHk9 :	-----			:
LpMDHk10 :	-----			:
LpMDHk11 :	CTCTTCGGGGTTTCCACCCCTGGATGTTGTCAGAGCTAACACACATTGTAGCTCA			: 801
LpMDHk12 :	-----			:
LpMDHk13 :	-----			:
LpMDHk14 :	-----			:
LpMDHk15 :	-----			:
LpMDHk16 :	-----			:
LpMDHk17 :	-----			:
LpMDHk18 :	CTCTTCGGGGTTTCCACCC			: 758
LpMDHk19 :	CTCTTCGGGGNTTNCACCCCTG			: 761
LpMDHk20 :	CTCTTCGGGGTTTCCACCCCTGGATGTTGTCAA			: 761
LpMDHk21 :	CTCTTCGGGGTTTCCACCCCTGGATGTTGTCAG			: 772
LpMDHk22 :	CTCTTCGGGGTTTCCACCCCTGGATGTTGTCAGAGCTAACACACATTGTAGCTCA			: 772
LpMDHk23 :	-----			: 800
LpMDHk24 :	-----			:
LpMDHk25 :	-----			:
LpMDHk26 :	-----			:
LpMDHk27 :	CTCTTCGGGGTTTCCACCCCTGGATGTTGTCAGA			: 771
LpMDHk28 :	CTCTTCGGGGTTTCCACCCCTGGATGTTGTCAGAG			: 773
LpMDHk29 :	-----			:
LpMDHk30 :	-----			:
LpMDHk31 :	-----			:
LpMDHk32 :	-----			:
LpMDHk33 :	-----			:
LpMDHk34 :	CTCTTCGGGGNTTACACCCCTGGATGTTGTC			: 764
LpMDHk35 :	CTCTTCGGGGNTTCCACCCCTGGATGTTGTCAGAGCTAACACACATTGTAGCT			: 785
LpMDHk36 :	-----			:
LpMDHk37 :	-----			:
LpMDHk38 :	-----			:
LpMDHk39 :	-----			:
LpMDHk40 :	-----			:
LpMDHk41 :	-----			:
LpMDHk42 :	CTCTTCGGGGTTTNCACCCCTGGATGTTGTCAGAGCTAACACACATTGTAGCTCA			: 786
LpMDHk43 :	-----			:
LpMDHk44 :	-----			:
LpMDHk45 :	-----			:
LpMDHk46 :	-----			:
LpMDHk47 :	-----			:
LpMDHk48 :	-----			:
LpMDHk49 :	-----			:
LpMDHk50 :	CTCTTCGGGGTTTC			: 741
LpMDHk51 :	-----			:
LpMDHk52 :	-----			:
LpMDHk53 :	CTCTTCGGGGTTTCCACCCCTGGATGTTGTCAGGGCTAACACACATT			: 770
LpMDHk54 :	-----			:
LpMDHk55 :	CTCTTCGGGGTTTCCACCCCTGGATGTTGTCAGGGCTAACACACATTGTAGCTCA			: 777
LpMDHk56 :	-----			:
LpMDHk57 :	-----			:
LpMDHk58 :	-----			:
LpMDHk59 :	-----			:
LpMDHk60 :	CTCTTCGGGGTTTCCACCCCTGGATGTTGTCAGAGCTAACACACATTGTAGCTCA			: 762
LpMDHk61 :	CTCTTC			: 701
LpMDHk62 :	-----			:
LpMDHk63 :	-----			:
LpMDHk64 :	-----			:
LpMDHk65 :	CTCTTCGGGGTTTCCACCCCTGGATGTTGTCAGAGCTAACACACATTGTAGCTCA			: 467
LpMDHk66 :	CTCTTCGGGGTTTCCACCCCTGGATGTTGTCAGAGCTAACACACATTGTAGCTCA			: 354

	*      860      *      880      *      900
LpMDHk1 :	-----
LpMDHk2 :	-----
LpMDHk3 :	-----
LpMDHk4 :	-----
LpMDHk5 :	-----
LpMDHk6 :	-----
LpMDHk7 :	-----
LpMDHk8 :	-----
LpMDHk9 :	-----
LpMDHk10 :	-----
LpMDHk11 :	A
LpMDHk12 :	-----
LpMDHk13 :	-----
LpMDHk14 :	-----
LpMDHk15 :	-----
LpMDHk16 :	-----
LpMDHk17 :	-----
LpMDHk18 :	-----
LpMDHk19 :	-----
LpMDHk20 :	-----
LpMDHk21 :	-----
LpMDHk22 :	AACCTC
LpMDHk23 :	-----
LpMDHk24 :	-----
) LpMDHk25 :	-----
LpMDHk26 :	-----
LpMDHk27 :	-----
LpMDHk28 :	-----
LpMDHk29 :	-----
LpMDHk30 :	-----
LpMDHk31 :	-----
LpMDHk32 :	-----
LpMDHk33 :	-----
LpMDHk34 :	-----
LpMDHk35 :	-----
LpMDHk36 :	-----
LpMDHk37 :	-----
LpMDHk38 :	-----
LpMDHk39 :	-----
LpMDHk40 :	-----
LpMDHk41 :	-----
LpMDHk42 :	AACCTCAGCTCATCGATGTTGATGTCCCAGTTGTCGGTGGCCATGCTGGGATCACGATT
LpMDHk43 :	-----
LpMDHk44 :	-----
LpMDHk45 :	-----
LpMDHk46 :	-----
LpMDHk47 :	-----
LpMDHk48 :	-----
LpMDHk49 :	-----
LpMDHk50 :	-----
LpMDHk51 :	-----
LpMDHk52 :	-----
LpMDHk53 :	-----
LpMDHk54 :	-----
LpMDHk55 :	-----
LpMDHk56 :	-----
LpMDHk57 :	-----
LpMDHk58 :	-----
LpMDHk59 :	-----
LpMDHk60 :	AACCT
LpMDHk61 :	-----
LpMDHk62 :	-----
LpMDHk63 :	-----
LpMDHk64 :	-----
LpMDHk65 :	AACCTCAGCCTCATCGATGTTGATGTCCCAGTTGTCGGTGGCCATGCTGGGATCACGATT
LpMDHk66 :	AACCTCAGCCTCATCGATGTTGATGTCCCAGTTGTCGGTGGCCATGCTGGGATCACGATT

	*	920	*	940	*	960
LpMDHk1 :						
LpMDHk2 :						
LpMDHk3 :						
LpMDHk4 :						
LpMDHk5 :						
LpMDHk6 :						
LpMDHk7 :						
LpMDHk8 :						
LpMDHk9 :						
LpMDHk10 :						
LpMDHk11 :						
LpMDHk12 :						
LpMDHk13 :						
LpMDHk14 :						
LpMDHk15 :						
LpMDHk16 :						
LpMDHk17 :						
LpMDHk18 :						
LpMDHk19 :						
LpMDHk20 :						
LpMDHk21 :						
LpMDHk22 :						
LpMDHk23 :						
LpMDHk24 :						
) LpMDHk25 :						
LpMDHk26 :						
LpMDHk27 :						
LpMDHk28 :						
LpMDHk29 :						
LpMDHk30 :						
LpMDHk31 :						
LpMDHk32 :						
LpMDHk33 :						
LpMDHk34 :						
LpMDHk35 :						
LpMDHk36 :						
LpMDHk37 :						
LpMDHk38 :						
LpMDHk39 :						
LpMDHk40 :						
LpMDHk41 :						
LpMDHk42 :						
LpMDHk43 :						
LpMDHk44 :						
LpMDHk45 :						
LpMDHk46 :						
) LpMDHk47 :						
LpMDHk48 :						
LpMDHk49 :						
LpMDHk50 :						
LpMDHk51 :						
LpMDHk52 :						
LpMDHk53 :						
LpMDHk54 :						
LpMDHk55 :						
LpMDHk56 :						
LpMDHk57 :						
LpMDHk58 :						
LpMDHk59 :						
LpMDHk60 :						
LpMDHk61 :						
LpMDHk62 :						
LpMDHk63 :						
LpMDHk64 :						
LpMDHk65 :	CTGCCTCTGTTGTCCAAGACTAGGCCTTCTGTCAGCTCACGGACGAGGAAACTGAACAG					: 587
LpMDHk66 :	CTGCCTCTGTTGTCCAAGACTAGGCCTTCTGTCAGCTCACGGACGAGGAAACTGAACAG					: 474

\* 980

\* 1000

\* 1020

LpMDHk1 :  
LpMDHk2 :  
LpMDHk3 :  
LpMDHk4 :  
LpMDHk5 :  
LpMDHk6 :  
LpMDHk7 :  
LpMDHk8 :  
LpMDHk9 :  
LpMDHk10 :  
LpMDHk11 :  
LpMDHk12 :  
LpMDHk13 :  
LpMDHk14 :  
LpMDHk15 :  
LpMDHk16 :  
LpMDHk17 :  
LpMDHk18 :  
LpMDHk19 :  
LpMDHk20 :  
LpMDHk21 :  
LpMDHk22 :  
LpMDHk23 :  
LpMDHk24 :  
) LpMDHk25 :  
LpMDHk26 :  
LpMDHk27 :  
LpMDHk28 :  
LpMDHk29 :  
LpMDHk30 :  
LpMDHk31 :  
LpMDHk32 :  
LpMDHk33 :  
LpMDHk34 :  
LpMDHk35 :  
LpMDHk36 :  
LpMDHk37 :  
LpMDHk38 :  
LpMDHk39 :  
LpMDHk40 :  
LpMDHk41 :  
LpMDHk42 :  
LpMDHk43 :  
LpMDHk44 :  
LpMDHk45 :  
LpMDHk46 :  
) LpMDHk47 :  
LpMDHk48 :  
LpMDHk49 :  
LpMDHk50 :  
LpMDHk51 :  
LpMDHk52 :  
LpMDHk53 :  
LpMDHk54 :  
LpMDHk55 :  
LpMDHk56 :  
LpMDHk57 :  
LpMDHk58 :  
LpMDHk59 :  
LpMDHk60 :  
LpMDHk61 :  
LpMDHk62 :  
LpMDHk63 :  
LpMDHk64 :  
LpMDHk65 : CTGACAAAGAGGATAACAGAACGCTGGACAGAGG|GGTGGAGGCGAA : 634  
LpMDHk66 : CTGACAAAGAGGATAACAGAACGCTGGACAGAGGCGGTGGAGGCGAAGGCTGG|TGCTGGC : 534

	*	1040	*	1060	*	1080
LpMDHk1	:	-	-	-	-	-
LpMDHk2	:	-	-	-	-	-
LpMDHk3	:	-	-	-	-	-
LpMDHk4	:	-	-	-	-	-
LpMDHk5	:	-	-	-	-	-
LpMDHk6	:	-	-	-	-	-
LpMDHk7	:	-	-	-	-	-
LpMDHk8	:	-	-	-	-	-
LpMDHk9	:	-	-	-	-	-
LpMDHk10	:	-	-	-	-	-
LpMDHk11	:	-	-	-	-	-
LpMDHk12	:	-	-	-	-	-
LpMDHk13	:	-	-	-	-	-
LpMDHk14	:	-	-	-	-	-
LpMDHk15	:	-	-	-	-	-
LpMDHk16	:	-	-	-	-	-
LpMDHk17	:	-	-	-	-	-
LpMDHk18	:	-	-	-	-	-
LpMDHk19	:	-	-	-	-	-
LpMDHk20	:	-	-	-	-	-
LpMDHk21	:	-	-	-	-	-
LpMDHk22	:	-	-	-	-	-
LpMDHk23	:	-	-	-	-	-
LpMDHk24	:	-	-	-	-	-
LpMDHk25	:	-	-	-	-	-
LpMDHk26	:	-	-	-	-	-
LpMDHk27	:	-	-	-	-	-
LpMDHk28	:	-	-	-	-	-
LpMDHk29	:	-	-	-	-	-
LpMDHk30	:	-	-	-	-	-
LpMDHk31	:	-	-	-	-	-
LpMDHk32	:	-	-	-	-	-
LpMDHk33	:	-	-	-	-	-
LpMDHk34	:	-	-	-	-	-
LpMDHk35	:	-	-	-	-	-
LpMDHk36	:	-	-	-	-	-
LpMDHk37	:	-	-	-	-	-
LpMDHk38	:	-	-	-	-	-
LpMDHk39	:	-	-	-	-	-
LpMDHk40	:	-	-	-	-	-
LpMDHk41	:	-	-	-	-	-
LpMDHk42	:	-	-	-	-	-
LpMDHk43	:	-	-	-	-	-
LpMDHk44	:	-	-	-	-	-
LpMDHk45	:	-	-	-	-	-
LpMDHk46	:	-	-	-	-	-
LpMDHk47	:	-	-	-	-	-
LpMDHk48	:	-	-	-	-	-
LpMDHk49	:	-	-	-	-	-
LpMDHk50	:	-	-	-	-	-
LpMDHk51	:	-	-	-	-	-
LpMDHk52	:	-	-	-	-	-
LpMDHk53	:	-	-	-	-	-
LpMDHk54	:	-	-	-	-	-
LpMDHk55	:	-	-	-	-	-
LpMDHk56	:	-	-	-	-	-
LpMDHk57	:	-	-	-	-	-
LpMDHk58	:	-	-	-	-	-
LpMDHk59	:	-	-	-	-	-
LpMDHk60	:	-	-	-	-	-
LpMDHk61	:	-	-	-	-	-
LpMDHk62	:	-	-	-	-	-
LpMDHk63	:	-	-	-	-	-
LpMDHk64	:	-	-	-	-	-
LpMDHk65	:	-	-	-	-	-
LpMDHk66	:	TCTGCTACTCTGTCCATGGCTTATGCCGCTGCCAGATTGTTGAGTCATCGCTCCGCGCA				: 594

	*	1100	*	1120	*	1140	
LpMDHk1 :	-	-	-	-	-	-	-
LpMDHk2 :	-	-	-	-	-	-	-
LpMDHk3 :	-	-	-	-	-	-	-
LpMDHk4 :	-	-	-	-	-	-	-
LpMDHk5 :	-	-	-	-	-	-	-
LpMDHk6 :	-	-	-	-	-	-	-
LpMDHk7 :	-	-	-	-	-	-	-
LpMDHk8 :	-	-	-	-	-	-	-
LpMDHk9 :	-	-	-	-	-	-	-
LpMDHk10 :	-	-	-	-	-	-	-
LpMDHk11 :	-	-	-	-	-	-	-
LpMDHk12 :	-	-	-	-	-	-	-
LpMDHk13 :	-	-	-	-	-	-	-
LpMDHk14 :	-	-	-	-	-	-	-
LpMDHk15 :	-	-	-	-	-	-	-
LpMDHk16 :	-	-	-	-	-	-	-
LpMDHk17 :	-	-	-	-	-	-	-
LpMDHk18 :	-	-	-	-	-	-	-
LpMDHk19 :	-	-	-	-	-	-	-
LpMDHk20 :	-	-	-	-	-	-	-
LpMDHk21 :	-	-	-	-	-	-	-
LpMDHk22 :	-	-	-	-	-	-	-
LpMDHk23 :	-	-	-	-	-	-	-
LpMDHk24 :	-	-	-	-	-	-	-
LpMDHk25 :	-	-	-	-	-	-	-
LpMDHk26 :	-	-	-	-	-	-	-
LpMDHk27 :	-	-	-	-	-	-	-
LpMDHk28 :	-	-	-	-	-	-	-
LpMDHk29 :	-	-	-	-	-	-	-
LpMDHk30 :	-	-	-	-	-	-	-
LpMDHk31 :	-	-	-	-	-	-	-
LpMDHk32 :	-	-	-	-	-	-	-
LpMDHk33 :	-	-	-	-	-	-	-
LpMDHk34 :	-	-	-	-	-	-	-
LpMDHk35 :	-	-	-	-	-	-	-
LpMDHk36 :	-	-	-	-	-	-	-
LpMDHk37 :	-	-	-	-	-	-	-
LpMDHk38 :	-	-	-	-	-	-	-
LpMDHk39 :	-	-	-	-	-	-	-
LpMDHk40 :	-	-	-	-	-	-	-
LpMDHk41 :	-	-	-	-	-	-	-
LpMDHk42 :	-	-	-	-	-	-	-
LpMDHk43 :	-	-	-	-	-	-	-
LpMDHk44 :	-	-	-	-	-	-	-
LpMDHk45 :	-	-	-	-	-	-	-
LpMDHk46 :	-	-	-	-	-	-	-
LpMDHk47 :	-	-	-	-	-	-	-
LpMDHk48 :	-	-	-	-	-	-	-
LpMDHk49 :	-	-	-	-	-	-	-
LpMDHk50 :	-	-	-	-	-	-	-
LpMDHk51 :	-	-	-	-	-	-	-
LpMDHk52 :	-	-	-	-	-	-	-
LpMDHk53 :	-	-	-	-	-	-	-
LpMDHk54 :	-	-	-	-	-	-	-
LpMDHk55 :	-	-	-	-	-	-	-
LpMDHk56 :	-	-	-	-	-	-	-
LpMDHk57 :	-	-	-	-	-	-	-
LpMDHk58 :	-	-	-	-	-	-	-
LpMDHk59 :	-	-	-	-	-	-	-
LpMDHk60 :	-	-	-	-	-	-	-
LpMDHk61 :	-	-	-	-	-	-	-
LpMDHk62 :	-	-	-	-	-	-	-
LpMDHk63 :	-	-	-	-	-	-	-
LpMDHk64 :	-	-	-	-	-	-	-
LpMDHk65 :	-	-	-	-	-	-	-
LpMDHk66 :	ATGGCTGGTGATCCAGATGTTACGAGTGCACGTATGTTAGTCAGTCTGAGTTAACAGAGCTT						654

	*	1160	*	1180	*	1200
LpMDHk1	:	-	-	-	-	-
LpMDHk2	:	-	-	-	-	-
LpMDHk3	:	-	-	-	-	-
LpMDHk4	:	-	-	-	-	-
LpMDHk5	:	-	-	-	-	-
LpMDHk6	:	-	-	-	-	-
LpMDHk7	:	-	-	-	-	-
LpMDHk8	:	-	-	-	-	-
LpMDHk9	:	-	-	-	-	-
LpMDHk10	:	-	-	-	-	-
LpMDHk11	:	-	-	-	-	-
LpMDHk12	:	-	-	-	-	-
LpMDHk13	:	-	-	-	-	-
LpMDHk14	:	-	-	-	-	-
LpMDHk15	:	-	-	-	-	-
LpMDHk16	:	-	-	-	-	-
LpMDHk17	:	-	-	-	-	-
LpMDHk18	:	-	-	-	-	-
LpMDHk19	:	-	-	-	-	-
LpMDHk20	:	-	-	-	-	-
LpMDHk21	:	-	-	-	-	-
LpMDHk22	:	-	-	-	-	-
LpMDHk23	:	-	-	-	-	-
LpMDHk24	:	-	-	-	-	-
} LpMDHk25	:	-	-	-	-	-
LpMDHk26	:	-	-	-	-	-
LpMDHk27	:	-	-	-	-	-
LpMDHk28	:	-	-	-	-	-
LpMDHk29	:	-	-	-	-	-
LpMDHk30	:	-	-	-	-	-
LpMDHk31	:	-	-	-	-	-
LpMDHk32	:	-	-	-	-	-
LpMDHk33	:	-	-	-	-	-
LpMDHk34	:	-	-	-	-	-
LpMDHk35	:	-	-	-	-	-
LpMDHk36	:	-	-	-	-	-
LpMDHk37	:	-	-	-	-	-
LpMDHk38	:	-	-	-	-	-
LpMDHk39	:	-	-	-	-	-
LpMDHk40	:	-	-	-	-	-
LpMDHk41	:	-	-	-	-	-
LpMDHk42	:	-	-	-	-	-
LpMDHk43	:	-	-	-	-	-
LpMDHk44	:	-	-	-	-	-
LpMDHk45	:	-	-	-	-	-
LpMDHk46	:	-	-	-	-	-
} LpMDHk47	:	-	-	-	-	-
LpMDHk48	:	-	-	-	-	-
LpMDHk49	:	-	-	-	-	-
LpMDHk50	:	-	-	-	-	-
LpMDHk51	:	-	-	-	-	-
LpMDHk52	:	-	-	-	-	-
LpMDHk53	:	-	-	-	-	-
LpMDHk54	:	-	-	-	-	-
LpMDHk55	:	-	-	-	-	-
LpMDHk56	:	-	-	-	-	-
LpMDHk57	:	-	-	-	-	-
LpMDHk58	:	-	-	-	-	-
LpMDHk59	:	-	-	-	-	-
LpMDHk60	:	-	-	-	-	-
LpMDHk61	:	-	-	-	-	-
LpMDHk62	:	-	-	-	-	-
LpMDHk63	:	-	-	-	-	-
LpMDHk64	:	-	-	-	-	-
LpMDHk65	:	-	-	-	-	-
LpMDHk66	:	CCATTCTCGCGTCCAGAGTTAAGCTGGAGGACGGNGTTGAGTCCATCATTTCTCC				714

	* 1220	* 1240	* 1260	
LpMDHk1 :	- - -	- - -	- - -	:
LpMDHk2 :	- - -	- - -	- - -	:
LpMDHk3 :	- - -	- - -	- - -	:
LpMDHk4 :	- - -	- - -	- - -	:
LpMDHk5 :	- - -	- - -	- - -	:
LpMDHk6 :	- - -	- - -	- - -	:
LpMDHk7 :	- - -	- - -	- - -	:
LpMDHk8 :	- - -	- - -	- - -	:
LpMDHk9 :	- - -	- - -	- - -	:
LpMDHk10 :	- - -	- - -	- - -	:
LpMDHk11 :	- - -	- - -	- - -	:
LpMDHk12 :	- - -	- - -	- - -	:
LpMDHk13 :	- - -	- - -	- - -	:
LpMDHk14 :	- - -	- - -	- - -	:
LpMDHk15 :	- - -	- - -	- - -	:
LpMDHk16 :	- - -	- - -	- - -	:
LpMDHk17 :	- - -	- - -	- - -	:
LpMDHk18 :	- - -	- - -	- - -	:
LpMDHk19 :	- - -	- - -	- - -	:
LpMDHk20 :	- - -	- - -	- - -	:
LpMDHk21 :	- - -	- - -	- - -	:
LpMDHk22 :	- - -	- - -	- - -	:
LpMDHk23 :	- - -	- - -	- - -	:
LpMDHk24 :	- - -	- - -	- - -	:
) LpMDHk25 :	- - -	- - -	- - -	:
LpMDHk26 :	- - -	- - -	- - -	:
LpMDHk27 :	- - -	- - -	- - -	:
LpMDHk28 :	- - -	- - -	- - -	:
LpMDHk29 :	- - -	- - -	- - -	:
LpMDHk30 :	- - -	- - -	- - -	:
LpMDHk31 :	- - -	- - -	- - -	:
LpMDHk32 :	- - -	- - -	- - -	:
LpMDHk33 :	- - -	- - -	- - -	:
LpMDHk34 :	- - -	- - -	- - -	:
LpMDHk35 :	- - -	- - -	- - -	:
LpMDHk36 :	- - -	- - -	- - -	:
LpMDHk37 :	- - -	- - -	- - -	:
LpMDHk38 :	- - -	- - -	- - -	:
LpMDHk39 :	- - -	- - -	- - -	:
LpMDHk40 :	- - -	- - -	- - -	:
LpMDHk41 :	- - -	- - -	- - -	:
LpMDHk42 :	- - -	- - -	- - -	:
LpMDHk43 :	- - -	- - -	- - -	:
LpMDHk44 :	- - -	- - -	- - -	:
LpMDHk45 :	- - -	- - -	- - -	:
LpMDHk46 :	- - -	- - -	- - -	:
LpMDHk47 :	- - -	- - -	- - -	:
LpMDHk48 :	- - -	- - -	- - -	:
LpMDHk49 :	- - -	- - -	- - -	:
LpMDHk50 :	- - -	- - -	- - -	:
LpMDHk51 :	- - -	- - -	- - -	:
LpMDHk52 :	- - -	- - -	- - -	:
LpMDHk53 :	- - -	- - -	- - -	:
LpMDHk54 :	- - -	- - -	- - -	:
LpMDHk55 :	- - -	- - -	- - -	:
LpMDHk56 :	- - -	- - -	- - -	:
LpMDHk57 :	- - -	- - -	- - -	:
LpMDHk58 :	- - -	- - -	- - -	:
LpMDHk59 :	- - -	- - -	- - -	:
LpMDHk60 :	- - -	- - -	- - -	:
LpMDHk61 :	- - -	- - -	- - -	:
LpMDHk62 :	- - -	- - -	- - -	:
LpMDHk63 :	- - -	- - -	- - -	:
LpMDHk64 :	- - -	- - -	- - -	:
LpMDHk65 :	- - -	- - -	- - -	:
LpMDHk66 :	GACCTGGAGGGAGTGACGGAGTACGAGGCCAAGGCCTTGANGCATTGAAGGCTGAGCTG			: 774

LpMDHk1 : --- : -  
LpMDHk2 : --- : -  
LpMDHk3 : --- : -  
LpMDHk4 : --- : -  
LpMDHk5 : --- : -  
LpMDHk6 : --- : -  
LpMDHk7 : --- : -  
LpMDHk8 : --- : -  
LpMDHk9 : --- : -  
LpMDHk10 : --- : -  
LpMDHk11 : --- : -  
LpMDHk12 : --- : -  
LpMDHk13 : --- : -  
LpMDHk14 : --- : -  
LpMDHk15 : --- : -  
LpMDHk16 : --- : -  
LpMDHk17 : --- : -  
LpMDHk18 : --- : -  
LpMDHk19 : --- : -  
LpMDHk20 : --- : -  
LpMDHk21 : --- : -  
LpMDHk22 : --- : -  
LpMDHk23 : --- : -  
LpMDHk24 : --- : -  
LpMDHk25 : --- : -  
LpMDHk26 : --- : -  
LpMDHk27 : --- : -  
LpMDHk28 : --- : -  
LpMDHk29 : --- : -  
LpMDHk30 : --- : -  
LpMDHk31 : --- : -  
LpMDHk32 : --- : -  
LpMDHk33 : --- : -  
LpMDHk34 : --- : -  
LpMDHk35 : --- : -  
LpMDHk36 : --- : -  
LpMDHk37 : --- : -  
LpMDHk38 : --- : -  
LpMDHk39 : --- : -  
LpMDHk40 : --- : -  
LpMDHk41 : --- : -  
LpMDHk42 : --- : -  
LpMDHk43 : --- : -  
LpMDHk44 : --- : -  
LpMDHk45 : --- : -  
LpMDHk46 : --- : -  
LpMDHk47 : --- : -  
LpMDHk48 : --- : -  
LpMDHk49 : --- : -  
LpMDHk50 : --- : -  
LpMDHk51 : --- : -  
LpMDHk52 : --- : -  
LpMDHk53 : --- : -  
LpMDHk54 : --- : -  
LpMDHk55 : --- : -  
LpMDHk56 : --- : -  
LpMDHk57 : --- : -  
LpMDHk58 : --- : -  
LpMDHk59 : --- : -  
LpMDHk60 : --- : -  
LpMDHk61 : --- : -  
LpMDHk62 : --- : -  
LpMDHk63 : --- : -  
LpMDHk64 : --- : -  
LpMDHk65 : --- : -  
LpMDHk66 : AAG : 777

Figure 38 Nucleotide sequence of LpMDH1

LpMDH1 : GNAAACAGNNNGCGNCTTTCCCTNCANTGTTGCCGTGCAATCGCTGANAAGTATCCAGAAA : 60  
          \*       20          \*       40          \*       60  
LpMDH1 : TCATATACGAGGAAGTAATTATTGATAACTGCTGTATGACGCTCGTGAAGAACCCCTGGTA : 120  
          \*       80          \*       100          \*       120  
LpMDH1 : CGTTTGATGTATTAGTGTATGCCAAATCTATATGGCGACATTATTAGTGTATGTGCTG : 180  
          \*       140          \*       160          \*       180  
LpMDH1 : GTTTGATCGGAGGCTGGGCCTAACTCCCAGCTGCAACATTGGTGAAGGTGGCATTGTC : 240  
          \*       200          \*       220          \*       240  
LpMDH1 : TTGCAGAGGCTGTCCATGGCTCTGCACCTGATATATCTGGCAAGAACCTGGCAAACCAA : 300  
          \*       260          \*       280          \*       300  
LpMDH1 : CTGCTCTTATGCTGAGTGCTGTTATGATGTTGCCACTTGCAATTNAACGACCAAGCAN : 360  
          \*       320          \*       340          \*       360  
LpMDH1 : AACGGATCCACAATGCTATCCTCCAGACTATCGNCAGGGGAAGNACANAAC TG : 414  
          \*       380          \*       400          \*

Figure 39 Deduced amino acid sequence of LpMDH1

\* 20 \* 40 \* 60  
LpMDH1 : KQXXLFXXCCRAIAKYPEIIYEEVIIDNCCMTLVKNPGTFDVLVMPNLYGDIISDLCAG : 60

\* 80 \* 100 \* 120  
LpMDH1 : LIGGLGLTPSCNIGEGGICLAEAVHGSAPDISGKNLANPTALMLSAVMMRLHQXNDQAX : 120

\*  
LpMDH1 : RIHNAILQTIKEGKXXT : 137

Figure 40 Nucleotide sequence of LpMDHm

\* 20 \* 40 \* 60  
LpMDHm : GNCACCNCAGNNACAACTCTGGTACCTCAATTGCTACTCCACACCTCACTACTCTACC : 60

\* 80 \* 100 \* 120  
LpMDHm : AATCCACTACACAGCTTCGAGCTACCCGCCCGCAATCAAACCTACCTCTCCCTAGCA : 120

\* 140 \* 160 \* 180  
LpMDHm : AATCTACAACATGAAGGCAGTCGTAGCTGGAGGCCGCCGGCATTGGACAGCCATTGTC : 180

\* 200 \* 220 \* 240  
LpMDHm : CCTCCTCTTAAGACCTGCCGCTCGTCACTGAGCTCGCCCTATACGATGTCGTCAACGC : 240

\* 260 \* 280 \* 300  
LpMDHm : CGTCGGTGTGCGACTGACCTCTCCACATCTCCTGCCCGCAAAGTAACCGGCTACCT : 300

\* 320 \* 340 \* 360  
LpMDHm : GCCGGCAAATGACGGTATGCAGCAGGCTCTCACTGGCGCCGACATCGTGGTCATCCCCGC : 360

\* 380 \* 400 \* 420  
LpMDHm : TGGTATTCCCCGCAAGCCCCGATGACCCGTGACGACCTTTCAAGATCAACGCCGGCAT : 420

\* 440 \* 460 \* 480  
LpMDHm : TGTCCAGGGTCTCATCGAGGGTGTGCCAAGCAGTGCCTCAAGGATACTGTTCTCGTCAT : 480

\* 500 \* 520 \* 540  
LpMDHm : CTCCAACCCGTCAACTCGACTGTGCCATGCCGCCGAGGTGCTGAAGAAGGCCGGTGT : 540

\* 560 \* 580 \* 600  
LpMDHm : CTTCGACCCCAAGAAGCTTCGGTGTCAACCACCTCGATGTCGTCCGCCGAGACCTT : 600

\* 620 \* 640 \*  
LpMDHm : CGTTGCCGAGATCACTGGCGAGAAGGACCCAGCGAAGTTGAACATNCCCGTA : 652

Figure 41 . Deduced amino acid sequence of LpMDHm

\* 20 \* 40 \* 60  
LpMDHm : XXPXTTLVPQLLLHTSLLLPIHYTASSYPAPAIQTTSP\*QIYNMKAVVAGAAGGIGQPLS : 59

\* 80 \* 100 \* 120  
LpMDHm : LLLKTCPLVTELALYDVVNAVGVATDLSHISSPAKVTGYLPANDGMQQALTGADIVVIPA : 119

\* 140 \* 160 \* 180  
LpMDHm : GIPRKPGMTRDDLFKINAGIVQGLIEGVAKHCPKAYVLVISNPVNSTVPIAAEVLKAGV : 179

\* 200 \*  
LpMDHm : FDPKKLFGVTTLDVVRAETFVAEITGEKDPAKLNXPV : 216

Figure 42 Nucleotide sequence of LpPEPCa

\* 20 \* 40 \* 60  
LpPEPCa : GNGTACACGAAATAGAATCAACGGAAAGCANGAAGTGATGATTGGGTATCAGCATTCTGG ; 60

\* 80 \* 100 \* 120  
LpPEPCa : GAAGGATGCTGGCCGTTCTCTGCTGGTTGGCACTTGTACAAAGCTCAAGAGGGAGCTTAT ; 120

\* 140 \* 160 \* 180  
LpPEPCa : TAAGGTTGCGGAGACGTTGGGGTTAAGNTGACTATGTTCATGGACGAGGGGGTACTGT ; 180

\* 200 \* 220 \* 240  
LpPEPCa : TGGAAAGAGGTGGCGGCCCTACCCATCTGCTATACTGTACAACCTCCAGATACTGTCCA ; 240

\* 260 \* 280 \* 300  
LpPEPCa : TGGATCACTTCGGTAACTGTTCAAGGTGAAGTCATTGAGCAGTCCTCGGAGAGGAGCA ; 300

\* 320 \* 340 \* 360  
LpPEPCa : TTTGTGTTTAGAACGCTCAACGTTTACAGCTGCTACTCTTGAACATGGTATGCATCC ; 360

\* 380 \* 400 \* 420  
LpPEPCa : ACCAATCTCACCTAACCAAGAACAGAATGGCGTGCTTGATGGATGAAATGGCTGTTGCCAC ; 420

\* 440 \* 460 \* 480  
LpPEPCa : AGAGGAATACCGTTCCATTGTTCCAAGAACCAAGATTGTTGAGTATTCCGCCTTGC ; 480

\* 500 \* 520 \* 540  
LpPEPCa : AACACCAGAGCTCGAGTATGGTAGGATGAATATTGAAGCAGGCCATCAAAACGTAAGCC ; 540

\* 560 \* 580 \* 600  
LpPEPCa : AAGCGGAGGAATCGAACATTGCGTGCAATTCTGGATATTGCTGGACACAGACTAG ; 600

\* 620 \* 640 \* 660  
LpPEPCa : ATTCCACCTGCCAGTGTGGCTTGNTTTGGTGCAGGCCATTCAAGCATGTCCTGCAAAGGA ; 660

\* 680 \* 700 \* 720  
LpPEPCa : CATTCGTANTCTCAAATCCTTCAGCAGATGTACAACGAGTGGCCGTTAGGGTTACCAT ; 720

\* 740 \* 760  
LpPEPCa : AAACCTGGTTGAGATGGTGGTGCAGGGCGATCCAGGTATAGCAGCT ; 76.9

Figure 43 Deduced amino acid sequence of LpPEPca

\* 20 \* 40 \* 60  
LpPEPca : XTRNRINGKXEV MIGYQHSGKDAGRFSAGWHL YKAQEELIKVAETFGVKXTMFHGRGGTV : 60

\* 80 \* 100 \* 120  
LpPEPca : GRGGGPTHLAILSQPPDTVHGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMHP : 120

\* 140 \* 160 \* 180  
LpPEPca : PISPKPEWRALMDEMAVVATEEYRSIVFQEPRFVEYFRLATPELEYGRMNIGSRPSKRKP : 180

\* 200 \* 220 \* 240  
LpPEPca : SGGIESLRAIPWIFAWTQTRFHLPVWLXFGAAFKHVLQKDIRXLQILQQMYNEWPFRVTI : 240

\*  
LpPEPca : NLVEMVFAKGDPGIAA : 256

Figure 44 Consensus contig nucleotide sequence of LpPEPCb

\* 20 \* 40 \* 60  
LpPEPCb : GAAGAAGTTGCTGATGTTTAAGNACATTNTGCCTTGCAGAGCTCCAGCAGATTGTT : 60

\* 80 \* 100 \* 120  
LpPEPCb : TTGGTGCTTACATCATCTCAATGGCAACTGCCCATCTGATGTGCTGTTGAGCTTT : 120

\* 140 \* 160 \* 180  
LpPEPCb : TGCAGCGGGAGTGCATATAAAAAAGCCATTGAGAGTTGTTCCACTATTGAAAAGCTTG : 180

\* 200 \* 220 \* 240  
LpPEPCb : CAGATCTTGAANCAGCTCCAGCATCTGTCACGACTATTTCATAGACTGGTACATGA : 240

\* 260 \* 280 \* 300  
LpPEPCb : ATAGAACATGGCAAGCAGGAGGTATGGATACTCAGACTCTGGAAAGGACGCTG : 300

\* 320 \* 340 \* 360  
LpPEPCb : GGCCTCTCTGCAGCGTGGCAAATGTATAAAGCACAAAGAACATCTCATAAAGGTGGCAA : 360

\* 380 \* 400 \* 420  
LpPEPCb : AGCAATATGGAGTAAAGTTAACATGTTCATGGAAGAGGTGGAACGGTTGGCAGAGGAG : 420

\* 440 \* 460 \* 480  
LpPEPCb : GTGGTCCCAGTCATCTGCTATATTATCTCAACCACCAAGACACGATAAAGGATCACTTC : 480

\* 500 \* 520 \* 540  
LpPEPCb : GTGTAACAGTTCAAGGCAGGGTCATAGAGCACTCATTGGAGAGGAACACTTGTGCTTC : 540

\* 560 \* 580 \* 600  
LpPEPCb : GAACTCTGCAACGTTCACTGCAGCTACTCTTGAGCATGGAATGCATCCTCCAATTTCAC : 600

\* 620 \* 640 \* 660  
LpPEPCb : CCAAGCCAGAATGGCGTGTATAATGGATGAGATGGCTGTAGTGGCAACAAAAGAACATTC : 660

\* 680 \* 700 \* 720  
LpPEPCb : GATCAATTGTCTTCCAAGAACCAACGTTTGTGAAATACTCCGCTGGCAACACCTGAGA : 720

\* 740 \* 760 \* 780  
LpPEPCb : CTGAATATGGTCGGATGAATATTGGTAGCCGGCCATCAAAGAGAAAGCCTAGTGGAGGCA : 780

\* 800 \* 820 \* 840  
LpPEPCb : TAGAATCGCTCCGTCAATTCCATGGATCTTGCTGGACACAGACAAGGTTCATCTTC : 840

\* 860 \* 880 \* 900  
LpPEPCb : CTGTATGGCTGGATTGGTGCAGCGTTCAAACATATCATGCAGAAGGACATCAGGAATA : 900

\* 920 \* 940 \* 960  
LpPEPCb : TCCATACTCTGAAAGAAATGTACAATGAGTGGCCATTCTTAGGGTCACCCCTGACTTGC : 960

\* 980 \* 1000 \* 1020  
LpPEPCb : TTGAGATGGTTTGCCAAGGGAGATCCAGGAATTGCTGCTTATATGACAAATTGCTTG : 1020

\* 1040 \* 1060 \* 1080  
LpPEPCb : TGTCTGAAGATCTGCAGCCCTTGGGGAGCAGCTGAGAAACAACCTTGAAAGAGACGAAAC : 1080

\* 1100 \* 1120 \* 1140  
LpPEPCb : AGTTACTCCTTCAGGTTGCTGCCACAAGGACGTTCTGAAGGGATCCTTACCTGAAGC : 1140

\* 1160 \* 1180 \* 1200  
LpPEPCb : AGCGTCTGCGGTGCGTGAGTCATACTACAAACATTGAATGTTGCCAAGCCNACACCC : 1200

\* 1220 \* 1240 \* 1260  
LpPEPCb : TGAAGCGGATAAGAGACCCTAGCTTCGAGGTGACACCGCAGCAGGCACCTCTGTCGAAGG : 1260

\* 1280 \* 1300 \* 1320  
LpPEPCb : AGTTCGCTGATGAGAAGGAGCCAGCTGAGCTGGTCAACTGAACCGTGGAGCGAGTACG : 1320

\* 1340 \* 1360 \* 1380  
LpPEPCb : CCCCAGGCCTGGAGGACACCTCATCCTTACCATGAAGGGTATTTGCTGTGAAATGCAA : 1380

\* 1400 \* 1420 \* 1440  
LpPEPCb : ACACAGGCTAGGCCAGTTGCCTATTGGAATAACTGTCATCCGTCAAGATGGGGCGTGA : 1440

\* 1460 \* 1480 \* 1500  
LpPEPCb : ATATGTGTGTTCCCCAAATGCTAGTGAACCCCTGGAGGCATTTGCCACTTACATGCCTT : 1500

\* 1520 \* 1540 \* 1560  
LpPEPCb : TTGGTTATGGATGNACTTGATCTTAATGNCAAGGGTTGAAAGCCTGATCTAAATAAA : 1560

\* 1580 \* 1600 \* 1620  
LpPEPCb : ATATGGAACAATGATATTCTGGTNGGATCTAATAATTGCTGGCTCTGGCATCGNAATA : 1620

\* 1640  
LpPEPCb : GNGATTGGAGTNGTTAAC : 1640

Figure 45 Deducing amino acid sequence of LpPEPCb

\* 20 \* 40 \* 60  
LpPEPCb : RSCXCFKXIXVLAELPADC<sup>GAYI</sup>ISMATAPSDVLAVELLQRECHIKKPLRVVPLFEKLA : 60

\* 80 \* 100 \* 120  
LpPEPCb : DLEXAPASVARLFSIDWYMN<sup>RING</sup>KQEV<sup>MIGY</sup>SDSGKDAGRLSAAWQMYKAQEDLIKVAK : 120

\* 140 \* 160 \* 180  
LpPEPCb : QYGVKLTMFHGRGGTVGRGGG<sup>PSHLAILSQPPDTI</sup>QGS<sup>LRTVQGEVIEH</sup>SFGEEHLCFR : 180

\* 200 \* 220 \* 240  
LpPEPCb : TLQRFTAATLEHGM<sup>HPPISPKPEWRAIMDEMAVVATKEYRSIVFQEPRFVEYFRSATPET</sup> : 240

\* 260 \* 280 \* 300  
LpPEPCb : EYGRMNIGSRPSKR<sup>KPSGGIESLRAIPWIFAWTQTRF</sup>HLPWLGF<sup>GAAFKHIMQKDIRNI</sup> : 300

\* 320 \* 340 \* 360  
LpPEPCb : HTLKEMYNEWPFFRVTLD<sup>LLEMVFAKGDPGIAALYDKLLVSEDLQPFGEQLRNNFEETKQ</sup> : 360

\* 380 \* 400 \* 420  
LpPEPCb : LLLQVAGHKDVLEGDPYLKQRLRLRESYITTLNVCQAXTLKRIRDPSFEVTPQQAPLSKE : 420

\* 440 \* 460  
LpPEPCb : FADEKEPAELVQLNRGSEYAPGLEDTLILTMKGICCGMQNTG : 462

Figure 46 Nucleotide sequences of nucleic acid fragments contributing to the consensus contig séquence LpPEPCb

	*	20	*	40	*	60	
LpPEPCb1	:	GAAGAAGTTGCTGATGTTAAGNACATTNTGCCTTGAGAGCTGGAGATTGTT					: 60
LpPEPCb2	:	-					:
LpPEPCb3	:	-					:
LpPEPCb4	:	-					:
LpPEPCb5	:	-					:
LpPEPCb6	:	-					:
	*	80	*	100	*	120	
LpPEPCb1	:	TTGGTGCTTACATCATCTCAATGGCAACTGCCCATCTGATGTGCTTGCTGAGCTT					: 120
LpPEPCb2	:	-					:
LpPEPCb3	:	-					:
LpPEPCb4	:	-					:
LpPEPCb5	:	-					:
LpPEPCb6	:	-					:
	*	140	*	160	*	180	
LpPEPCb1	:	TGCAGCGGGAGTGCCATATAAAAAAGCCATTGAGAGTTGTTCCACTATTGAAAAGCTTG					: 180
LpPEPCb2	:	-					:
LpPEPCb3	:	-					:
LpPEPCb4	:	-					:
LpPEPCb5	:	-					:
LpPEPCb6	:	-					:
	*	200	*	220	*	240	
LpPEPCb1	:	CAGATCTTGAANCAGCTCAGCAGTCAGACTATTCAATAAGACTGGTACATGA					: 240
LpPEPCb2	:	-					:
LpPEPCb3	:	-					:
LpPEPCb4	:	-					:
LpPEPCb5	:	-					:
LpPEPCb6	:	-					:
	*	260	*	280	*	300	
LpPEPCb1	:	ATAGAACATGGCAAGCAGGAGGTATGATTGGATACTCAGACTCTGGAAAGGACGCTG					: 300
LpPEPCb2	:	-					:
LpPEPCb3	:	-					:
LpPEPCb4	:	-					:
LpPEPCb5	:	-					:
LpPEPCb6	:	-					:
	*	320	*	340	*	360	
LpPEPCb1	:	GGCGTCTCTGCAGCGTGGCAAATGTATAAACGACAAGAACATCTGATAAAAGGTGGCAA					: 360
LpPEPCb2	:	-	GTATAAACGACAAGAACATCTGATAAAAGGTGGCAA				: 35
LpPEPCb3	:	-					:
LpPEPCb4	:	-					:
LpPEPCb5	:	-					:
LpPEPCb6	:	-					:
	*	380	*	400	*	420	
LpPEPCb1	:	AGCAATATGGAGTAAAGTTAACATGTTCATGGAAGAGGTGGAACGGTGGCAGAGGAG					: 420
LpPEPCb2	:	AGCAATATGGAGTAAAGTTAACATGTTCATGGAAGAGGTGGAACGGTGGCAGAGGAG					: 95
LpPEPCb3	:	-	AATGTTT	GTGGAAGAGGTGGAACGGTGGCAGAGGAG			: 37
LpPEPCb4	:	-		-	GCAAGGAG		: 9
LpPEPCb5	:	-					:
LpPEPCb6	:	-					:

	*            440            *	*            460            *	*            480	
LpPEPCb1	: GTGGTCCCAGTCATCTTGTATATTATCTAACCAACCAAGACACGATAACAAGGATCACTTC			: 480
LpPEPCb2	: GTGGTCCCAGTCATCTTGTATATTATCTAACCAACCAAGACACGATAACAAGGATCACTTC			: 155
LpPEPCb3	: GTGGTCCCAGTCATCTTGTATATTATCTAACCAACCAAGACACGATAACAAGGATCACTTC			: 97
LpPEPCb4	: GTGGTCCCAGTCATCTTGTATATTATCTAACCAACCAAGACACGATAACAAGGATCACTTC			: 69
LpPEPCb5	: -----			: -
LpPEPCb6	: -----			: -
	*            500            *	*            520            *	*            540	
LpPEPCb1	: GTGTAACAGTTCAAGGCAGGTCATAGAGCACTCATTGGAGAGGAACACTTGTGCTTCA			: 540
LpPEPCb2	: GTGTAACAGTTCAAGGCAGGTCATAGAGCACTCATTGGAGGGAAACACTTGTGCTTCA			: 215
LpPEPCb3	: GTGTAACAGTTCAAGGCAGGTCATAGAGCACTCATTGGAGAGGAACACTTGTGCTTCA			: 157
LpPEPCb4	: GTGTAACAGTTCAAGGCAGGTCATAGAGCACTCATTGGAGAGGAACACTTGTGCTTCA			: 129
LpPEPCb5	: -----			: -
LpPEPCb6	: -----			: -
	*            560            *	*            580            *	*            600	
LpPEPCb1	: GAACTCTGCAACGTTTCACTGCAGCTACTCTTGAGCATGGAATGCATCCTCCAATTTCAC			: 600
LpPEPCb2	: GAACTCTGCAACGTTTCACTGCAGCTACTCTTGAGCATGGAATGCATCCTCCAATTTCAC			: 275
LpPEPCb3	: GAACTCTGCAACGTTTCACTGCAGCTACTCTTGAGCATGGAATGCATCCTCCAATTTCAC			: 217
LpPEPCb4	: GAACTCTGCAACGTTTCACTGCAGCTACTCTTGAGCATGGAATGCATCCTCCAATTTCAC			: 189
LpPEPCb5	: -----			: -
LpPEPCb6	: -----			: -
	*            620            *	*            640            *	*            660	
LpPEPCb1	: CCAA <del>CC</del> CAGAAATGGC <del>CC</del> TGCTATAATGGATGA <del>ATGG</del> CTGTAG <del>GG</del> CA <del>GG</del> AAAAGAA <del>AT</del> TC			: 660
LpPEPCb2	: CCAAGCCAGAAATGGCGTGTATAATGGATGAGATGGCTGTAGTGGCAACAAAAGAAATATC			: 335
LpPEPCb3	: CCAAGCCAGAAATGGCGTGTATAATGGATGAGATGGCTGTAGTGGCAACAAAAGAAATATC			: 277
LpPEPCb4	: CCAAGCCAGAAATGGCGTGTATAATGGATGAGATGGCTGTAGTGGCAACAAAAGAAATATC			: 249
LpPEPCb5	: -----			: -
LpPEPCb6	: -----			: -
	*            680            *	*            700            *	*            720	
LpPEPCb1	: GATCAATTGNC <del>CC</del> TTCCAAGAAC <del>CC</del> NNTTTGNC <del>CC</del> AAATA			: 697
LpPEPCb2	: GATCAATTGTCTTCCAAGAAC <del>CC</del> ACGTTTGTCGA <del>AA</del> ACTTCCGCTCGGCAACACCTGAGA			: 395
LpPEPCb3	: GATCAATTGTCTTCCAAGAAC <del>CC</del> ACGTTTGTCGA <del>AA</del> ACTTCCGCTCGGCAACACCTGAGA			: 337
LpPEPCb4	: GATCAATTGTCTTCCAAGAAC <del>CC</del> ACGTTTGTCGA <del>AA</del> ACTTCCGCTCGGCAACACCTGAGA			: 309
LpPEPCb5	: -----			: -
LpPEPCb6	: -----			: -
	*            740            *	*            760            *	*            780	
LpPEPCb1	: -----			: -
LpPEPCb2	: CTGAATATGGTCGGATGA <del>AT</del> TTGGTAGGCCGGCATCAAAGAGAAAGCCTAGTGGAGGCA			: 455
LpPEPCb3	: CTGAATATGGTCGGATGA <del>AT</del> TTGGTAGGCCGGCATCAAAGAGAAAGCCTAGTGGAGGCA			: 397
LpPEPCb4	: CTGAATATGGTCGGATGA <del>AT</del> TTGGTAGGCCGGCATCAAAGAGAAAGCCTAGTGGAGGCA			: 369
LpPEPCb5	: -----			: -
LpPEPCb6	: -----			: -
	*            800            *	*            820            *	*            840	
LpPEPCb1	: -----			: -
LpPEPCb2	: TAGAATCGCTCCGTGCAATTCCATGGATCTTGCTTGGACACAGAC <del>AG</del> GTTTCATCTTC			: 515
LpPEPCb3	: TAGAATCGCTCCGTGCAATTCCATGGATCTTGCTTGGACACAGAC <del>AG</del> GTTTCATCTTC			: 457
LpPEPCb4	: TAGAATCGCTCCGTGCAATTCCATGGATCTTGCTTGGACACAGAC <del>AG</del> GTTTCATCTTC			: 429
LpPEPCb5	: -----			: -
LpPEPCb6	: -----			: -

	*        860        *	880	*	900	
LpPEPCb1 :	- - - - -				
LpPEPCb2 :	CTGTATGGCTTGATTGGTGCAGCGTTCAACATATCATGCAGAAGGACATCAGGAATA				: 575
LpPEPCb3 :	CTGTATGGCTTGATTGGTGCAGCGTTCAACATATCATGCAGAAGGACATCAGGAATA				: 517
LpPEPCb4 :	CTGTATGGCTTGATTGGTGCAGCGTTCAACATATCATGCAGAAGGACATCAGGAATA				: 489
LpPEPCb5 :	- - - - -				: -
LpPEPCb6 :	- - - - -				: -
	*        920        *	940	*	960	
LpPEPCb1 :	- - - - -				: -
LpPEPCb2 :	TCCATACTCTGAAAGAAATGTACAATGAGTGGCCATTCTTAGGGTCACCCTTGACTTGC				: 635
LpPEPCb3 :	TCCATACTCTGAAAGAAATGTACAATGAGTGGCCATTCTTAGGGTCACCCTTGACTTGC				: 577
LpPEPCb4 :	TCCATACTCTGAAAGAAATGTACAATGAGTGGCCATTCTTAGGGTCACCCTTGACTTGC				: 549
LpPEPCb5 :	- - - - -				: -
LpPEPCb6 :	- - - - -				: -
	*        980        *	1000	*	1020	
LpPEPCb1 :	- - - - -				: -
LpPEPCb2 :	TTGAGATGGTTTGCAAGGGAGATCCAGGAATTGCTGCTTTATATGACAAATTGCTTG				: 695
LpPEPCb3 :	TTGAGATGGTTTGCAAGGGAGATCCAGGAATTGCTGCTTTATATGACAAATTGCTTG				: 637
LpPEPCb4 :	TTGAGATGGTTTGCAAGGGAGATCCAGGAATTGCTGCTTTATATGACAAATTGCTTG				: 609
LpPEPCb5 :	- - - - - GGTGTTTG-CNAGGGAGATCC-GG-ATTGCTGCTTTATATGACAAATTGCTTG				: 50
LpPEPCb6 :	- - - - -				: -
	*        1040        *	1060	*	1080	
LpPEPCb1 :	- - - - -				: -
LpPEPCb2 :	TGTCTGAAGATCTGCAGCCCTTGGGGAGCAGCTGA <del>N</del> AAACAAC <del>T</del> TGAAGAGACGAAAC				: 755
LpPEPCb3 :	TGTCTGAAGATCTGCAGCCCTTGGGGAGCAGCTGA <del>G</del> AAACAAC <del>T</del> TGAAGAGACGAAAC				: 697
LpPEPCb4 :	TGTCTGAAGATCTGCAGCCCTTGGGGAGCAGCTGA <del>G</del> AAACAAC <del>T</del> TGAAGAGACGAAAC				: 669
LpPEPCb5 :	TGTCTGAAGATCTGCAGCCCTTGGGGAGCAGCTGA <del>G</del> AAACAAC <del>T</del> TGAAGAGACGAAAC				: 110
LpPEPCb6 :	- - - - -				: -
	*        1100        *	1120	*	1140	
LpPEPCb1 :	- - - - -				: -
LpPEPCb2 :	AGNTACTCTTAAGGTTGTCGCCACAA <del>G</del> GG				: 785
LpPEPCb3 :	AGTTACTCCTTCAGGTTGCTGCCACAA <del>G</del> GGACGTTCTTGAAGGGGATCCTTACCTGAAGC				: 757
LpPEPCb4 :	AGTTACTCCTTCAGGTTGCTGCCACAA <del>G</del> GGACGTTCTTGAAGGGGATCCTTACCTGAAGC				: 729
LpPEPCb5 :	AGTTACTCCTTCAGGTTGCTGCCACAA <del>G</del> GGACGTTCTTGAAGGGGATCCTTACCTGAAGC				: 170
LpPEPCb6 :	- - - - - GGACGTTCTTGAAGGGGATCCTTACCTGAAGC				: 32
	*        1160        *	1180	*	1200	
LpPEPCb1 :	- - - - -				: -
LpPEPCb2 :	- - - - -				: -
LpPEPCb3 :	AGCGTCTGCGG <del>G</del> TGCGTGAGTCATAC				: 783
LpPEPCb4 :	AGCGTCTGCGGTTGCGTGAGTCATACATCACAA <del>C</del> CA				: 764
LpPEPCb5 :	AGCGTCTGCGGTTGCGTGAGTCATACATCACAA <del>C</del> ATTGAATGTTGCCAAGC <del>C</del> ACACCC				: 230
LpPEPCb6 :	AGCGTCTGCGGTTGCGTGAGTCATACATCACAA <del>C</del> ATTGAATGTTGCCAAGC <del>C</del> NNCACCC				: 92
	*        1220        *	1240	*	1260	
LpPEPCb1 :	- - - - -				: -
LpPEPCb2 :	- - - - -				: -
LpPEPCb3 :	- - - - -				: -
LpPEPCb4 :	- - - - -				: -
LpPEPCb5 :	TGAAGCGGATAAGAGACCC <del>T</del> AGCTCGAGGTGACACCGCAGCAGGCACCTCTGTCGAAGG				: 290
LpPEPCb6 :	TGAAGCGGATAAGAGACCC <del>T</del> AGCTCGAGGTGACACCGCAGCAGGCACCTCTGTCGAAGG				: 152

	*      1280	*      1300	*      1320	
LpPEPCb1	:	- - -	- - -	:
LpPEPCb2	:	- - -	- - -	:
LpPEPCb3	:	- - -	- - -	:
LpPEPCb4	:	- - -	- - -	:
LpPEPCb5	:	AGTTCGCTGATGAGAAGGAGCCAGCTGAGCTGGTGCAACTGAACCGTGGGAGCGAGTACG		: 350
LpPEPCb6	:	AGTTCGCTGATGAGAAGGAGCCAGCTGAGCTGGTGCAACTGAACCGTGGGAGCGAGTACG		: 212
	*      1340	*      1360	*      1380	
LpPEPCb1	:	- - -	- - -	:
LpPEPCb2	:	- - -	- - -	:
LpPEPCb3	:	- - -	- - -	:
LpPEPCb4	:	- - -	- - -	:
LpPEPCb5	:	CCCCAGGCCTGGAGGACACCCTCATCCTTACCATGAAGGGTA-TTGC[FGTGGAAATGCAA		: 409
LpPEPCb6	:	CCCCAGGCCTGGAGGACACCCTCATCCTTACCATGAAGGGTATTGCFGTGGAAATGCAA		: 272
	*      1400	*      1420	*      1440	
LpPEPCb1	:	- - -	- - -	:
LpPEPCb2	:	- - -	- - -	:
LpPEPCb3	:	- - -	- - -	:
LpPEPCb4	:	- - -	- - -	:
LpPEPCb5	:	ACACAGGCTAGGCCAGTTGCCATA-TTGGAAATAACTGTCAT[CCGTCAGATGGGGCGTGA		: 468
LpPEPCb6	:	ACACAGGCTAGGCCAGTTGCCATA-TTGGAAATAACTGTCATCCCCTGCAAGAT-GGGCGTGA		: 331
	*      1460	*      1480	*      1500	
LpPEPCb1	:	- - -	- - -	:
LpPEPCb2	:	- - -	- - -	:
LpPEPCb3	:	- - -	- - -	:
LpPEPCb4	:	- - -	- - -	:
LpPEPCb5	:	ATATGTGTGTTCCCCAAATGCTAGTGAACCTGGAGGCATTTGGCCTACATGCCTT		: 528
LpPEPCb6	:	ATATGTGTGTTCCCCAAATGCTAGTGAACCTGGAGGCATTTGGCCTACATGCCTT		: 390
	*      1520	*      1540	*      1560	
LpPEPCb1	:	- - -	- - -	:
LpPEPCb2	:	- - -	- - -	:
LpPEPCb3	:	- - -	- - -	:
LpPEPCb4	:	- - -	- - -	:
LpPEPCb5	:	TTGGTTATGNATGNAC-TTGATCTTAATGNCAAGGGTTGTTGAAGCCTGATCTAAATAAA		: 587
LpPEPCb6	:	TTGGTTATGGATGNACTTGATCTTAATG[CAANGGTTGTTGAAGCCTGATCTAAATNAA		: 450
	*      1580	*      1600	*      1620	
LpPEPCb1	:	- - -	- - -	:
LpPEPCb2	:	- - -	- - -	:
LpPEPCb3	:	- - -	- - -	:
LpPEPCb4	:	- - -	- - -	:
LpPEPCb5	:	ATATGGAACAATGATATTCTGG-NGGATCTAATAATTGCTTGGCTGTGGCATCGNAATA		: 646
LpPEPCb6	:	ATATGGAACAATGATATTCTGGTGTCTTA		: 482
	*      1640			
LpPEPCb1	:	- - -	- - -	:
LpPEPCb2	:	- - -	- - -	:
LpPEPCb3	:	- - -	- - -	:
LpPEPCb4	:	- - -	- - -	:
LpPEPCb5	:	GNGATTGGAGTNGTTAAC	: 666	
LpPEPCb6	:	- - -	- - -	:

Figure 47 Nucleotide sequence of LpPEPCC

\* 20 \* 40 \* 60  
LpPEPCC : AGCANTCTGTNCTTNCCANCAACCACGTTTGTNCGAATACTTNCCGCTCGGCAACACCT : 60

\* 80 \* 100 \* 120  
LpPEPCC : GCACACTGAATATGGTCGGCATGAATATTGGTAGCCGGCCATCAAAGAGAAAGCCTAGTG : 120

\* 140 \* 160 \* 180  
LpPEPCC : GAGGCATAGAATCGCTCCGTGCAATTCCATGCATCTTGNTTGGACACAGACAAGGNTN : 180

\* 200 \* 220  
LpPEPCC : ATNTTCCTGTATGNCTTGNATTGNCTCCACCNCACCCCCNTA : 224

Figure 48 Deduced amino acid sequence of LpPEPCC

\* 20 \* 40 \* 60  
LpPEPCC : XSXLXXNHVLXEYXPLGNTCTLNMVGMNIGSRPSKRKPSGGIESLRAIIPCIFXWTQTRXX : 60

\*  
LpPEPCC : XPVXLXFNSTXTP : 73

Figure 49 Nucleotide sequence of LpPEPCd

\* 20 \* 40 \* 60  
LpPEPCd : GTTNCTGGAACNAAGGATCTTCTTGAAAGGTGATCCCTACCTGAAGCAGCGGCTCCGCCTC : 60

\* 80 \* 100 \* 120  
LpPEPCd : CGTGACGCGTACATCACCAACCATGAACGTATGCCAGGCCTACACATTGAAGCGGATCCGT : 120

\* 140 \* 160 \* 180  
LpPEPCd : GACCCAGACTACCACGTGCACTGCGGCCCATCTTCCAAGGAGGTTATGGACACAAGC : 180

\* 200 \* 220 \* 240  
LpPEPCd : AAGCCGGCTTCGAGCTTGTGACGCTGAACCCGGCCAGCGAGTACGCCCGGGCTGGAG : 240

\* 260 \* 280 \* 300  
LpPEPCd : GACACCCCTCATCTTGACCATGAAGGGCGTTGCTGCCGGTCTGCAAAACACCGGTTAGGGC : 300

\* 320 \* 340 \* 360  
LpPEPCd : CAGGAGAGATGCCGTGATCACCATCTTTGTATCTTCATGATGATGCGATGTTTTCTTT : 360

\* 380 \* 400 \* 420  
LpPEPCd : AGTCGTTGCGGTGGCCTATATCTCTCGGACGTAGCTGCATCTGTCTCCCTGCTCAGT : 420

\* 440 \* 460 \* 480  
LpPEPCd : GAGGAATAATGGCGTTGCCCAAGTATATTGATAAAAGGAACCGATGTTAATTTC : 480

\* 500 \* 520  
LpPEPCd : AGATTGTTGTTAGTAATTGTTCTATTTATTTGCGAAAAAAAAAAA : 527

Figure 50 Deduced amino acid sequence of LpPEPCd

\* 20 \* 40 \* 60  
LpPEPCd : VXGXKDLLEGDPYLKQRLRLDAYITTMNVQCQAYTLKRIRD**P**DYHVALRPHLSKEVMDTS : 60

\* 80 \*  
LpPEPCd : KPASELVTLNPASEYAPGLEDTLILTMKGVAAGLQNTG : 98

Figure 51 Nucleotide sequence of LpPEPc<sup>e</sup>

\* 20 \* 40 \* 60  
LpPEPc<sup>e</sup> : GTTACACCGCGCAGTTGCTTAGCAAGGNAGATGGCTGCTAACTTGTACTTCTCTCAG : 60

\* 80 \* 100 \* 120  
LpPEPc<sup>e</sup> : ATAGAAGATCTGATGTTGAGCTCTCTATGTGGCGCTGCAGTGATGAACTTAGGGTCCGT : 120

\* 140 \* 160 \* 180  
LpPEPc<sup>e</sup> : GCAGATGAAGTACATCTGTCCTCAAAAAAAAATCTGCAAAGCATTACATAGAGTTCTGG : 180

\* 200 \* 220 \* 240  
LpPEPc<sup>e</sup> : AAGCAAGTTCCCTCAAATGAACCTTATCGTGTCACTTGGCGATGTCAGGGATAAACTG : 240

\* 260 \* 280 \* 300  
LpPEPc<sup>e</sup> : TACTATACGCGCGAACGTTCTGCCACATATTGACAACGGAAATTTCAGACATTCCAGAA : 300

\* 320 \* 340 \* 360  
LpPEPc<sup>e</sup> : GNGTCAACTTTACTAATGTAACGTGTTCTGGAACCTCTTGAGCTGTGCTACAGATCC : 360

\* 380 \* 400 \* 420  
LpPEPc<sup>e</sup> : TTATCTTNCTGTGGNGACAAANCTATTGCTGANGGAAGCCTCTTGATTCTNGCGNNCN : 420

\* 440 \*  
LpPEPc<sup>e</sup> : GNATCNACTTTGTGGCTTACTCTNGCGAA : 450

Figure 52 Deduced amino acid sequence of LpPEPc

\* 20 \* 40 \* 60  
LpPEPc : VTRAVCLLARXMAANLYFSQIEDLMFELSMWRCSDELRVRADEVHLSSKKSAKHYIEFW : 60

\* 80 \* 100 \* 120  
LpPEPc : KQVPPNEPYRVLGDVRDKLYYTRERSRHILTTGISDIPEXSTFTNVELFLEPLELCYRS : 120

\* 140 \*  
LpPEPc : LSXCXDKXIAKGSLDFXXXXTLWAYSXE : 150

Figure 53 Nucleotide sequence of LpPEPCf

LpPEPCf : GGGGTGGTGGCCCTNCTCACCTTGCCTNCCTGTCANCCACCAGNCACAATCAACGGAT : 60  
             \*       20             \*       40             \*       60  
LpPEPCf : CACTCCGGGTGACTGTTCAAGGTGAAGTTATTGAGCAGAGCTTGGGAGGAACACTTGT : 120  
             \*       80             \*       100             \*       120  
LpPEPCf : GCTTCAGGACGCTGCAGCGTTCACAGCTGCTACTCTTGAGCATGGATGCGTCCACCCA : 180  
             \*       140             \*       160             \*       180  
LpPEPCf : TTTCACCAAAGCCAGAGTGGCGAGCTCTTCTTGATGAGATGGCTGTGGTTGCAACTGAGG : 240  
             \*       200             \*       220             \*       240  
LpPEPCf : AATAACCGGTCAATCGTCTTCCAAGAACCAACGCTTCGTCGAGTATTCCGCCCTGCAACAC : 300  
             \*       260             \*       280             \*       300  
LpPEPCf : CAGAGACAGAGTATGGCAGGATGAATATAGGAAGCAGGCCATCAAAGAGAAAACCAAGTG : 360  
             \*       320             \*       340             \*       360  
LpPEPCf : GTGGCATTGAATCACTCCGTGCAATTCCATGGATCTTCGCATGGACGCAGACACGGTTCC : 420  
             \*       380             \*       400             \*       420  
LpPEPCf : ACCTTCCAGTCTGGTTGGCTTGGTGGTGCATTCAAGCATATCCTCAAGAAGGACATCA : 480  
             \*       440             \*       460             \*       480  
LpPEPCf : GAAATTCCATATGCTCCAGGAGATGTACAACGAGTGGCCATTTTCAGGGTCACGATCG : 540  
             \*       500             \*       520             \*       540  
LpPEPCf : ATCTTGTTGAGATGGTGGTGCACAGGAGCTACAGCCACTGGGTGACAAGCTGAGG : 600  
             \*       560             \*       580             \*       600  
LpPEPCf : TCCTGGTTTCAGAGGAGCTACAGCCACTGGGTGACAAGCTGAGG : 644  
             \*       620             \*       640

Figure 54 Deduced amino acid sequence of LpPEPCf

\* 20 \* 40 \* 60  
LpPEPCf : GGGPXHLAXLSXPPXTINGSLRVTVQGEVIEQSFGEEHLCFRTLQRFTAATLEHGMRPPI : 60

\* 80 \* 100 \* 120  
LpPEPCf : SPKPEWRALLDEMAVVATEEYRSIVFQEPRFVEYFRLATPETEYGRMNIGSRPSKRKPSG : 120

\* 140 \* 160 \* 180  
LpPEPCf : GIESLRAIPWIFAWTQTRFHLPVWLGFGGAFKHILKKDIRNFHMLQEMYNEWPFFRVTID : 180

\* 200 \*  
LpPEPCf : LVEMVFAKGNGIAALYDRLLVSEELQPLGDKLR : 214

Figure 55 Consensus contig nucleotide sequence of TrMDHa

\* 20 \* 40 \* 60  
TrMDHa : GGCTTCTTAAAAACNCACTAAACTCTTTCTATTGTTCTTATTCCTCGATCTATTCCA : 60

\* 80 \* 100 \* 120  
TrMDHa : ATGGCCAAAGACCCAGTCGTGTTCTGCACTGGTGCTGCAGGACAAATTGGGTATGCT : 120

\* 140 \* 160 \* 180  
TrMDHa : CTTGTCCCTATGATTGCTAGGGGAGTGATGCTCGGCCCTGACCAGCCTGTGATCCTCCAC : 180

\* 200 \* 220 \* 240  
TrMDHa : ATGCTTGACATTCCACCTGCAGCCGAATCACTAACGGTGTAAAATGGAGTTGGTGGAT : 240

\* 260 \* 280 \* 300  
TrMDHa : GCTGCATTCCCTCTTAAAGGAGTTGGCTACAACGTGATGTGGTTGAGGCATGCACT : 300

\* 320 \* 340 \* 360  
TrMDHa : GGTGTCAATAATTGCCGTATGGTGGGGTCCCTAGAAAAGAAGGTATGGAGAGGAAA : 360

\* 380 \* 400 \* 420  
TrMDHa : GATGTGATGACAAAAATGTCTCTATTACAAGTCTCAGGCTTCTGCCCTTGAAAAACAT : 420

\* 440 \* 460 \* 480  
TrMDHa : GCTGCTGCAAATGCAAGGTTCTTGTGTTGCCAACCCAGCAAACACCAATGCATTGATC : 480

\* 500 \* 520 \* 540  
TrMDHa : TTGAAGGAATATGCTCCATCCATTCTGAGAAAAACATTCTGCTTGACTAGATTGGAC : 540

\* 560 \* 580 \* 600  
TrMDHa : CATAACAGGGCACTAGGTCAAATTCTGAAAGACTAAACGTTGAAGTTCTGATGTGAAA : 600

\* 620 \* 640 \* 660  
TrMDHa : AATGTTATAATATGGGGAAATNATTCAACTCAATAACCTGNTGTNAACCACNCAAC : 660

\*  
TrMDHa : CGTTAAAATCTCCT : 674

Figure 56 Deduced amino acid sequence of TrMDHa

\* 20 \* 40 \* 60  
TrMDHa : MAKDPVRVLVTGAAGQIGYALVPMIARGVMLGPDQPVILHMLDIPPAESLNGVKMELVD : 60

\* 80 \* 100 \* 120  
TrMDHa : AAFPLLKGVVATTDVVEACTGVNIAVMVGGFPRKEGMERKDVMTKNVSIYKSQASALEKH : 120

\* 140 \* 160 \* 180  
TrMDHa : AAANCKVLVVANPANTNALILKEYAPSipeknisalTRLDHNRALGQISERLNVEVSDVK : 180

\* 200  
TrMDHa : NVIIWGKXFINSIPXCXPXNR : 201

Figure 57 Nucleotide sequences of nucleic acid fragments contributing to the consensus contig sequence TrMDHa

	*	20	*	40	*	60	:
TrMDHa1	:	GINTTCTTNAACNCNCTAAINTCTTTCTATTGTNCTNNNTTCTCGATCTATTCCA					60
TrMDHa2	:	-GCNACNTAIAAACGCACTNTNCTNAGCTCTATTGTCTTATTCGATCTATTCCA					59
TrMDHa3	:	-GCNTCTTAAAAC-CACTAAACTCTTTCTATTGTCTTATTCGATCTATTCCA					57
TrMDHa4	:	-GCNTCTTAAAAC-CACTAAACTCTTTCTATTGTCTTATTCGATCTATTCCA					57
TrMDHa5	:	--CTTCTTAAAAC-CACTAAACTCTTTCTATTGTCTTATTCGATCTATTCCA					55
TrMDHa6	:	--CNIAAAACNCACTAAACTCTTTCTATTGTCTTATTCGATCTATTCCA					54
TrMDHa7	:	--GCNTAAAACCTTTCTATTGTCTTATTCGATCTATTCCA					45
TrMDHa8	:	--GCNTAAAACCTTTCTATTGTCTTATTCGATCTATTCCA					45
TrMDHa9	:	--CACTAAACTCTTTCTATTGTCTTATTCGATCTATTCCA					41
TrMDHa10	:	--TAAACTCTTCTATTGTCTTATTCGATCTATTCCA					41
TrMDHa11	:	--AAACCTTTCTATTGTCTTATTCGATCTATTCCA					41
	*	80	*	100	*	120	:
TrMDHa1	:	ATGGCCAAAGACCCAGTCGTTCTGTCCTGGTGCTGCAGGACAAGTTGGGTATGCT					120
TrMDHa2	:	ATGGCCAAAGACCCAGTCGTTCTGTCCTGGTGCTGCAGGACAATTGGGTATGCT					119
TrMDHa3	:	ATGGCCAAAGACCCAGTCGTTCTGTCCTGGTGCTGCAGGACAATTGGGTATGCT					117
TrMDHa4	:	ATGGCCAAAGACCCAGTCGTTCTGTCCTGGTGCTGCAGGACAATTGGGTATGCT					117
TrMDHa5	:	ATGGCCAAAGACCCAGTCGTTCTGTCCTGGTGCTGCAGGACAATTGGGTATGCT					115
TrMDHa6	:	ATGGCCAAAGACCCAGTCGTTCTGTCCTGGTGCTGCAGGACAATTGGGTATGCT					114
TrMDHa7	:	ATGGCCAAAGACCCAGTCGTTCTGTCCTGGTGCTGCAGGACAATTGGGTATGCT					104
TrMDHa8	:	ATGGCCAAAGACCCAGTCGTTCTGTCCTGGTGCTGCAGGACAATTGGGTATGCT					103
TrMDHa9	:	ATGGCCAAAGACCCAGTCGTTCTGTCCTGGTGCTGCAGGACAATTGGGTATGCT					99
TrMDHa10	:	ATGGCCAAAGACCCAGTCGTTCTGTCCTGGTGCTGCAGGACAATTGGGTATGCT					100
TrMDHa11	:	ATGGCCAAAGACCCAGTCGTTCTGTCCTGGTGCTGCAGGACAATTGGGTATGCT					101
	*	140	*	160	*	180	:
TrMDHa1	:	CTTGTCCCTATGATTGCTAGGGGAGTGTGCTCGGNCCTGACCAANGTGTGATCCTNCAC					180
TrMDHa2	:	CTTGTCCCTATGATTGCTAGGGGAGTGTGCTCGGCCCTGACCAGCGCTGTGATCCTCCAC					179
TrMDHa3	:	CTTGTCCCTATGATTGCTAGGGGAGTGTGCTCGGCCCTGACCAGCGCTGTGATCCTCCAC					177
TrMDHa4	:	CTTGTCCCTATGATTGCTAGGGGAGTGTGCTCGGCCCTGACCAGCGCTGTGATCCTCCAC					177
TrMDHa5	:	CTTGTCCCTATGATTGCTAGGGGAGTGTGCTCGGCCCTGACCAGCGCTGTGATCCTCCAC					175
TrMDHa6	:	CTTGTCCCTATGATTGCTAGGGGAGTGTGCTCGGCCCTGACCAGCGCTGTGATCCTCCAC					174
TrMDHa7	:	CTTGTCCCTATGATTGCTAGGGGAGTGTGCTCGGCCCTGACCAGCGCTGTGATCCTCCAC					164
TrMDHa8	:	CTTGTCCCTATGATTGCTAGGGGAGTGTGCTCGGCCCTGACCAGCGCTGTGATCCTCCAC					163
TrMDHa9	:	CTTGTCCCTATGATTGCTAGGGGAGTGTGCTCGGCCCTGACCAGCGCTGTGATCCTCCAC					159
TrMDHa10	:	CTTGTCCCTATGATTGCTAGGGGAGTGTGCTCGGCCCTGACCAGCGCTGTGATCCTCCAC					160
TrMDHa11	:	CTTGTCCCTATGATTGCTAGGGGAGTGTGCTCGGCCCTGACCAGCGCTGTGATCCTCCAC					161
	*	200	*	220	*	240	:
TrMDHa1	:	ATGCTTGACATTNCACCTGAG-----					202
TrMDHa2	:	ATGCTTGACATTCACCTGCAGCCGAATCACTAACGGTGTAAAATGGAGTTGGTGGAT					239
TrMDHa3	:	ATGCTTGACATTCCACCTGCAGCCGAATCACTAACGGTGTAAAATGGAGTTGGTGGAT					237
TrMDHa4	:	ATGCTTGACATTCCACCTGCAGCCGAATCACTAACGGTGTAAAATGGAGTTGGTGGAT					237
TrMDHa5	:	ATGCTTGACATTCCACCTGCAGCCGAATCACTAACGGTGTAAAATGGAGTTGGTGGAT					235
TrMDHa6	:	ATGCTTGACATTCCACCTGCAGCCGAATCACTAACGGTGTAAAATGGAGTTGGTGGAT					234
TrMDHa7	:	ATGCTTGACATTCCACCTGCAGCCGAATCACTAACGGTGTAAAATGGAGTTGGTGGAT					224
TrMDHa8	:	ATGCTTGACATTCCACCTGCAGCCGAATCACTAACGGTGTAAAATGGAGTTGGTGGAT					223
TrMDHa9	:	ATGCTTGACATTCCACCTGCAGCCGAATCACTAACGGTGTAAAATGGAGTTGGTGGAT					219
TrMDHa10	:	ATGCTTGACATTCCACCTGCAGCCGAATCACTAACGGTGTAAAATGGAGTTGGTGGAT					220
TrMDHa11	:	ATGCTTGACATTCCACCTGCAGCCGAATCACTAACGGTGTAAAATGGAGTTGGTGGAT					221

\* 260 \* 280 \* 300

TrMDHa1	:	- - -	-	-
TrMDHa2	:	GCTGCATTCCCTCTTAAAGGAGTTGTTGCTAC	ACTGATGTGGT	TGAGGCATGCACT
TrMDHa3	:	GCTGCATTCCCTCTTAAAGGAGTTGTTGCTACA	ACTGATGTGGT	TGAGGCATGCACT
TrMDHa4	:	GCTGCATTCCCTCTTAAAGGAGTTGTTGCTACA	ACTGATGTGGT	TGAGGCATGCACT
TrMDHa5	:	GCTGCATTCCCTCTTAAAGGAGTTGTTGCTACA	ACTGATGTGGT	TGAGGCATGCACT
TrMDHa6	:	GCTGCATTCCCTCTTAAAGGAGTTGTTGCTACA	ACTGATGTGGT	TGAGGCATGCACT
TrMDHa7	:	GCTGCATTCCCTCTTAAAGGAGTTGTTGCTACA	ACTGATGTGGT	TGAGGCATGCACT
TrMDHa8	:	GCTGCATTCCCTCTTAAAGGAGTTGTTGCTACA	ACTGATGTGGT	TGAGGCATGCACT
TrMDHa9	:	GCTGCATTCCCTCTTAAAGGAGTTGTTGCTACA	ACTGATGTGGT	TGAGGCATGCACT
TrMDHa10	:	GCTGCATTCCCTCTTAAAGGAGTTGTTGCTACA	ACTGATGTGGT	TGAGGCATGCACT
TrMDHa11	:	GCTGCATTCCCTCTTAAAGGAGTTGTTGCTACA	ACTGATGTGGT	TGAGGCATGCACT

\* 320 \* 340 \* 360

TrMDHa1	:	- - -	-	-
TrMDHa2	:	GG@GTCAATATTGCCGTTATGGTTGGG	GGGTTCCCTAGAAAAGAAGGTATGGAGAGGAAA	: 359
TrMDHa3	:	GGTGTCAATATTGCCGTTATGGTTGGGTTCCCTAGAAAAGAAGGTATGGAGAGGAAA	: 357	
TrMDHa4	:	GGTGTCAATATTGCCGTTATGGTTGGGTTCCCTAGAAAAGAAGGTATGGAGAGGAAA	: 357	
TrMDHa5	:	GGTGTCAATATTGCCGTTATGGTTGGGTTCCCTAGAAAAGAAGGTATGGAGAGGAAA	: 355	
TrMDHa6	:	GGTGTNAATATTGACGNATGGNTGGNGGGTTMCNTAGANACAA	GTNT-----	: 344
TrMDHa7	:	GGTGTCAATATTGCCGTTATGGTTGGGTTCCCTAGAAAAGAAGGTATGGAGAGGAAA	: 344	
TrMDHa8	:	GGTGTCAATATTGCCGTTATGGTTGGGTTCCCTAGAAAAGAAGGTATGGAGAGGAAA	: 343	
TrMDHa9	:	GGTGTCAATATTGCCGTTATGGTTGGGTTCCCTAGAAAAGAAGGTATGGAGAGGAAA	: 339	
TrMDHa10	:	GGTGTCAATATTGCCGTTATGGTTGGGTTCCCTAGAAAAGAAGGTATGGAGAGGAAA	: 340	
TrMDHa11	:	GGTGTCAATATTGCCGTTATGGTTGGGTTCCCTAGAAAAGAAGGTATGGAGAGGAAA	: 341	

\* 380 \* 400 \* 420

TrMDHa1	:	- - -	-	-
TrMDHa2	:	GATGTGATGACAAAAAAATGTCTCTATTACAAGTCTCAGGCTTCTGCCTTGAAAAACAT	: 419	
TrMDHa3	:	GATGTGATGACAAAAAAATGTCTCTATTACAAGTCTCAGGCTTCTGCCTTGAAAAACAT	: 417	
TrMDHa4	:	GATGTGATGACAAAAAAATGTCTCTATTACAAGTCTCAGGCTTCTGCCTTGAAAAACAT	: 417	
TrMDHa5	:	GATGTGATGACAAAAAAATGTCTCTATTACAAGTCTCAGGCTTCTGCCTTGAAAAACAT	: 415	
TrMDHa6	:	- - -	-	-
TrMDHa7	:	GATGTGATGACAAAAAAATGTCTCTATTACAAGTCTCAGGCTTCTGCCTTGAAAAACAT	: 404	
TrMDHa8	:	GATGTGATGACAAAAAAATGTCTCTATTACAAGTCTCAGGCTTCTGCCTTGAAAAACAT	: 403	
TrMDHa9	:	GATGTGATGACAAAAAAATGTCTCTATTACAAGTCTCAGGCTTCTGCCTTGAAAAACAT	: 399	
TrMDHa10	:	GATGTGATGACAAAAAAATGTCTCTATTACAAGTCTCAGGCTTCTGCCTTGAAAAACAT	: 400	
TrMDHa11	:	GATGTGATGACAAAAAAATGTCTCTATTACAAGTCTCAGGCTTCTGCCTTGAAAAACAT	: 400	

\* 440 \* 460 \* 480

TrMDHa1	:	- - -	-	-
TrMDHa2	:	GCTGCTGAAACTGCAAGGTTCTGTTGCTAACCCAGCAAACACCAATGCATTGATC	: 479	
TrMDHa3	:	GCTGCTGAAACTGCAAGGTTCTGTTGCTAACCCAGCAAACACCAATGCATTGATC	: 477	
TrMDHa4	:	GCTGCTGAAACTGCAAGGTTCTGTTGCTAACCCAGCAAACACCAATGCATTGATC	: 477	
TrMDHa5	:	GCTGCTGAAACTGCAAGGTTCTGTTGCTAACCCAGCAAACACCAATGCATTGATC	: 475	
TrMDHa6	:	- - -	-	-
TrMDHa7	:	GCTGCTGAAACTGCAAGGTTCTGTTGCTAACCCAGCAAACACCAATGCATTGATC	: 464	
TrMDHa8	:	GCTGCTGAAACTGCAAGGTTCTGTTGCTAACCCAGCAAACACCAATGCATTGATC	: 463	
TrMDHa9	:	GCTGCTGAAACTGCAAGGTTCTGTTGCTAACCCAGCAAACACCAATGCATTGATC	: 459	
TrMDHa10	:	GCTGCTGAAACTGCAAGGTTCTGTTGCTAACCCAGCAAACACCAATGCATTGATC	: 460	
TrMDHa11	:	GCTGCTGAAACTGCAAGGTTCTGTTGCTAACCCAGCAAACACCAATGCATTGATC	: 460	

\* 500 \* 520 \* 540

TrMDHa1	:	-----	-----	-----	:	-
TrMDHa2	:	TTGAAGGAATATGCTCCATCCATTCTGAGAAAAACATTCTGCTTGTACTAGATTGGAC			:	539
TrMDHa3	:	TTGAAGGAATATGCTCCATCCATTCTGAGAAAAACATTCTGCTTGTACTAGATTGGAC			:	537
TrMDHa4	:	TTGAAGGAATATGCTCCATCCATTCTGAGAAAAACATTCTGCTTGTACTAGATTGGAC			:	537
TrMDHa5	:	TTGAAGGAATATGCTCCATCCATTCTGAGAAAAACATTCTGCTTGTACTAGATTGGAC			:	535
TrMDHa6	:	-----	-----	-----	:	-
TrMDHa7	:	TTGAAGGAATATGCTCCATCCATTCTGAGAAAAACATTCTGCTTGTACTAGATTGGAC			:	524
TrMDHa8	:	TTGAAGGAATATGCTCCATCCATTCTGAGAAAAACATTCTGCTTGTACTAGATTGGAC			:	523
TrMDHa9	:	TTGAAGGAATATGCTCCATCCATTCTGAGAAAAACATTCTGCTTGTACTAGATTGGAC			:	519
TrMDHa10	:	TTGAAGGAATATGCTCCATCCATTCTGAGAAAAACATTCTGCTTGTACTAGATTGGAC			:	520
TrMDHa11	:	TTGAAGGAATATGCTCCATCCATTCTGAGAAAAACATTCTGCTTGTACTAGATTGGAC			:	520

\* 560 \* 580 \* 600

TrMDHa1	:	-----	-----	-----	:	-
TrMDHa2	:	CATAACAGGGCACTGGTCA-----			:	559
TrMDHa3	:	CATAACAGGGCACTAGGTCAAATTCTGAA-----			:	567
TrMDHa4	:	CATAACAGGGCACTAGGTCAAATTCTGAAAGACTAAA-----			:	575
TrMDHa5	:	CATAACAGGGCACTAGGTCAAATTCTGAAAGACTAAACGTTGAAGTTCTGATGTGAAA			:	595
TrMDHa6	:	-----	-----	-----	:	-
TrMDHa7	:	CATAACAGGGCACTAGGTCAAATTCTGAAAGAC-----			:	558
TrMDHa8	:	CATAACAGGGCACTAGGTCAAATTCTGAAAGACTAAACGTTGAAGTTCTGATGTGAAA			:	583
TrMDHa9	:	CATAACAGGGCACTAGGTCAAATTCTGAAAGACTAAACGTTGAAGTTCTGATGTGAA-----			:	577
TrMDHa10	:	CATAACAGGGCACTAGGTCAAATTCTGAAAGACTAAACGTTGAAGTTCTGATGTGAAA			:	580
TrMDHa11	:	CATAACAGGGCACTAGGGCAAATTNTGAAAAGACTAAACGTTGAAGTTNTGATGTGAAA			:	580

\* 620 \* 640 \* 660

TrMDHa1	:	-----	-----	-----	:	-
TrMDHa2	:	-----	-----	-----	:	-
TrMDHa3	:	-----	-----	-----	:	-
TrMDHa4	:	-----	-----	-----	:	-
TrMDHa5	:	AATGTTAT-A-AT-----			:	606
TrMDHa6	:	-----	-----	-----	:	-
TrMDHa7	:	-----	-----	-----	:	-
TrMDHa8	:	AATGTTATAATGTGG-----			:	599
TrMDHa9	:	-----	-----	-----	:	-
TrMDHa10	:	AATGTTATAATGTG-----			:	594
TrMDHa11	:	AATGTTATATATGGGGAAATNATTCACTCAACTAACCTGNTGTNAACCACNCAAC			:	639

\*

TrMDHa1	:	-----	:	:
TrMDHa2	:	-----	:	:
TrMDHa3	:	-----	:	:
TrMDHa4	:	-----	:	:
TrMDHa5	:	-----	:	:
TrMDHa6	:	-----	:	:
TrMDHa7	:	-----	:	:
TrMDHa8	:	-----	:	:
TrMDHa9	:	-----	:	:
TrMDHa10	:	-----	:	:
TrMDHa11	:	CGTTAAAATCTCCT	:	653

Figure 58 Consensus contig nucleotide sequence of TrMDHb

TrMDHb :	* 20 * 40 * 60 TTCTCCCANAATCNNGAAANGCCCACATCACACAACATAACACCTTACTCTNCTTTC : 60
TrMDHb :	* 80 * 100 * 120 TCTCTNAACAAAACGTTCTCCTCTCTTAATCTCCCTGTTGATTCCCTTCCATTCT : 120
TrMDHb :	* 140 * 160 * 180 TCAAAAAATGCCAAAGACCCAGTTCGTGTCTCGTCACTGGTGCTGCAGGGCAAATTGGT : 180
TrMDHb :	* 200 * 220 * 240 TATGCACTTGTCCCTATGATTGCTAGGGAGTGATGCTGGTCCTGATCAACCTGTGATC : 240
TrMDHb :	* 260 * 280 * 300 CTTCACATGCTTGAATTCCCTCCAGCAGCAGAGTCATTGAATGGAGTTAACATGGAGTTG : 300
TrMDHb :	* 320 * 340 * 360 GTCGATGCTGCATTCCACTTCTAAAGGTGTTGCTACAACGTGATGTTGAAGCA : 360
TrMDHb :	* 380 * 400 * 420 TGCACGGAGTCATATTGCAGTCATGGTTGGTGGATTCCCAAGAAAAGAAGGTATGGAG : 420
TrMDHb :	* 440 * 460 * 480 AGGAAGGATGTGATGTCTAAGAACGTCTCTATTACAAGTCCCAGGCTCTGCCCTTGAA : 480
TrMDHb :	* 500 * 520 * 540 AAGCATGCTGCCAACTGCAAGGTTTGGTTGCTAACCCAGCAAACACCAATGCA : 540
TrMDHb :	* 560 * 580 * 600 TTGATCTTGAAGGAATTGCTCCATCTATTCCAGAGAAAACATTCTTGTGACTAGA : 600
TrMDHb :	* 620 * 640 * 660 CTTGATCACAAACAGGGCATTGGGCCAATTCTGAAAGATTGAATGTTCAAGTTCTGAT : 660
TrMDHb :	* 680 * 700 * 720 GTAAAGAATGTCATTATCTGGGTAATCATTCAACTCAGTATCCTGATGTCAACCAT : 720
TrMDHb :	* 740 * 760 * 780 GCAACTGTTAACACCCCCGCTGGGAGAACGCTGTCGTGAGCTTGTGATGACGCC : 780
TrMDHb :	* 800 * 820 * 840 TGGTTGAATGGAGAATTCATATCTACCGTTCAACAAACGTGGTGCTGCAATTATTAAGGCT : 840
TrMDHb :	* 860 * 880 * 900 AGAAAGCTTCAAGCGCACTATCCGCTGCTAGCGCTGCTGCGACCACATTGCGATTGG : 900
TrMDHb :	* 920 * 940 * 960 GTTCTGGAACTCCCCAGGGCACCTCGTTCAATGGGAGTGTATTCTGATGGTTCTTAC : 960

\* 980 \* 1000 \* 1020  
TrMDHb : AACGTACCAGCTGGACTCATCTATTCAATTCCCTGTCACCACTGCTAATGGGAATGGAAA : 1020

\* 1040 \* 1060 \* 1080  
TrMDHb : ATTGTTCAAGGACTTCAATTGACGAGTTCTCAAGGAAGAAGTTGGACTTGACAGCTGAA : 1080

\* 1100 \*  
TrMDHb : GAGTTATCCGAGGAAAAGAGTTGGCATACT : 1111

Figure 59 Deduced amino acid sequence of TrMDHb

\* 20 \* 40 \* 60

TrMDHb : MAKDPVRVLVTGAAGQIGYALVPMIARGVMLGPDQPVILHMLDIPPAESLNGVKMELVD : 60

\* 80 \* 100 \* 120

TrMDHb : AAFPLLKGVVATTDVVEACTGVNIAVMVGGFPRKEGMERKDVMMSNVIYKSQASALEKH : 120

\* 140 \* 160 \* 180

TrMDHb : AAANCKVLVVANPANTNALILKEFAPSipeKNISCLTRLDHNRALGQISERLNQVSDVK : 180

\* 200 \* 220 \* 240

TrMDHb : NVIIWGNHSSTQYPDVNHATVNTPAGEKPVRELVSDDAWLNGEFISTVQORGAAIIKARK : 240

\* 260 \* 280 \* 300

TrMDHb : LSSALSAASAACDHIRDWVLGTPQGTFVSMGVYSDGSYNVPAGLIYSFPVTTANGEWKIV : 300

\* 320

TrMDHb : QGLSIDESRKKLDLTAEELSEEKSLAY : 328

Figure 60 Nucleotide sequences of nucleic acid fragments contributing to the consensus contig sequence TrMDHb

	*	20	*	40	*	60	
TrMDHb1	:	TTCTCCCNAATCNNGAAANC	NCGG	ACA	CA	AC	: 47
TrMDHb2	:	TTCTCNCANAATCNNGAAANC	CCGG	A-A	A	AC	: 45
TrMDHb3	:	-GNNACGAGAA	CACA	ACA	CA	TAA	: 37
TrMDHb4	:	-GTC	NTCA	ACA	CA	ACA	: 32
TrMDHb5	:	-GCNCANACAT	ACACAACACTAAACCT	NA	CT	-NCTC	: 35
TrMDHb6	:	-GCAA	ACA	CA	ACA	C-TAA	: 27
TrMDHb7	:	-TTC	ACG	TA	ACC	C-TAN	: 28
TrMDHb8	:	-G-NA	CCACCC	TAAC	CCTGACTNN	C-TNC	: 25
TrMDHb9	:	-GA	NGC	TC	ACT	-A-C-TNC	: 16
TrMDHb10	:	-CAN	ACTAAACG	TA	CT	CNGAC	: 21
TrMDHb11	:	-CAAAGA	CACT	AACT	AC	TNC	: 21
TrMDHb12	:	-AACAGTAACCC	TA	CTNCTGTC			: 22
TrMDHb13	:	-CN	TAAC	CCTNACTCN	C-T-C		: 18
TrMDHb14	:	-TCA	TC	ACT	N-C	TNC	: 14
TrMDHb15	:	-CACTAAACCT	NN	CTNCTGTC			: 20
TrMDHb16	:	-GNAACGACNTAAA	ACTNC				: 20
TrMDHb17	:	-ACCACNTAACGCT	-CCTNC				: 18
TrMDHb18	:	-A-CACNT	AAAGCTNC	TNC			: 16
TrMDHb19	:	-CTAN	GCT	CACTC			: 12
TrMDHb20	:	-GCA	T-C	TC			: 7
TrMDHb21	:	-	-	-	-	-	: 4
TrMDHb22	:	-	-	-	-	-	: 2
TrMDHb23	:	-	-	-	-	-	
TrMDHb24	:	-	-	-	-	-	
TrMDHb25	:	-	-	-	-	-	
TrMDHb26	:	-	-	-	-	-	
TrMDHb27	:	-	-	-	-	-	
TrMDHb28	:	-	-	-	-	-	
TrMDHb29	:	-	-	-	-	-	
TrMDHb30	:	-	-	-	-	-	
TrMDHb31	:	-	-	-	-	-	
TrMDHb32	:	-	-	-	-	-	

		*	80	*	100	*	120	:	
TrMDHb1	:	TCT	-----AAACAAAAGTCTCTCTTAATCTCCCTGTTGATTCCCTCCA-GTTCT					: .104	
TrMDHb2	:	TCT	-----AAACAAAAGTCTCTCTTAATCTCCCTGTTGATTCCCTCCA-GTTCT					: .102	
TrMDHb3	:	TMA	-----AACAAAAAGTCTCTCTTAATCTCCCTGTTGATTCCCTCCA-GTTCT					: .94	
TrMDHb4	:	TCT	-----NAAACAAAANGCTATCTCTCATCTCTTAATCTCCCTGTTGATTCCCTCCA-GTTCT					: .91	
TrMDHb5	:	TCT	-----NAAACAAAAGCTATCTCTCATCTCTTAATCTCCCTGTTGATTCCCTCCA-GTTCT					: .91	
TrMDHb6	:	TCT	-----AAACAAAAGCTATCTCTCATCTCTTAATCTCCCTGTTGATTCCCTCCA-GTTCT					: .84	
TrMDHb7	:	TNN	-----AACAAAAAGCTATCTCTNATCTCTTAATCTCCCTGTTGATTCCCTCCA-GTTCT					: .85	
TrMDHb8	:	TCT	-----NAAACAAAAGCTATCTCTCATCTCTTAATCTCCCTGTTGATTCCCTCCA-GTTCT					: .84	
TrMDHb9	:	TCA	-----AACAAAAAGCTATCTCTCATCTCTTAATCTCCCTGTTGATTCCCTCCA-GTTCT					: .72	
TrMDHb10	:	TCTCA	-----AAC-AAAACTGNTCTCTCTCTTAATCTCCCTGTTGATTCCCTCCA-GTTCT					: .78	
TrMDHb11	:	TCTCTNAAC	-----AAAAGTCTCTCTCTTAATCTCCCTGTTGATTCCCTCCA-GTTCT					: .80	
TrMDHb12	:	TCTCT	-----NAAACAAAAGTCTCTCTCTTNAATCTCCCTGTTGATTCCCTCCA-GTTCT					: .81	
TrMDHb13	:	TCT	-----NAAACAAAAGCTATCTTNAATCTCTTAATCTCCCTGTTGATTCCCTCCA-GTTCT					: .75	
TrMDHb14	:	TNC	-----AAACAAAAGCTCTCTCATCTCTTAATCTCCCTGTTGATTCCCTCCA-GTTCT					: .71	
TrMDHb15	:	TCTCT	-----AAACAAAAGCTCTCTCTTNAATCTCCCTGTTGATTCCCTCCA-GTTCT					: .79	
TrMDHb16	:	TCTCTNAAC	-----AAAAGTCTCTCTCTTNAATCTCCCTGTTGATTCCCTCCA-GTTCT					: .78	
TrMDHb17	:	TCT	-----C-AACAAAAAGCTGTCTC-GCTCTTAATCTCCCTGTTGATTCCCTCCA-GTTCT					: .76	
TrMDHb18	:	TCTCT	-----AAC-AAAACTGTTCTCTCTCTTAATCTCCCTGTTGATTCCCTCCA-GTTCT					: .74	
TrMDHb19	:	TCT	-----NNAACAAAAGCTGTCTC-GCTCTTAATCTCCCTGTTGATTCCCTCCA-GTTCT					: .70	
TrMDHb20	:	TMA	-----AACAAAAAGCTGTCTC-GCTCTTAATCTCCCTGTTGATTCCCTCCA-GTTCT					: .63	
TrMDHb21	:	CCTCTNAAC	-----AACAAAAGCTGTCTC-GCTTNAATCTCCCTGTTGATTCCCTCCA-GTTCT					: .63	
TrMDHb22	:	TCT	-----NAACAAAAGCTGTCTC-GCTCTTNAATCTCCCTGTTGATTCCCTCCA-GTTCT					: .59	
TrMDHb23	:	-	-----CAAAAGTCTCTCTCTTNAATCTCCCTGTTGATTCCCTCCA-GTTCT					: .51	
TrMDHb24	:	-	-----AAAAGTCTCTCTCTTNAATCTCCCTGTTGATTCCCTCCA-GTTCT					: .49	
TrMDHb25	:	-	-----GNNTTCTCTCTCTTNAATCTCCCTGTTGATTCCCTCCA-GAGTTCTCCA-GTTCT					: .46	
TrMDHb26	:	-	-----EGTTCTC-GCTCTTAATCTCCCTGTTGATTCCCTCCA-GTTCT					: .44	
TrMDHb27	:	-	-----TTCCTCTCTTNAATCTCCCTGTTGATTCCCTCCA-GTTCT					: .39	
TrMDHb28	:	-						:	-
TrMDHb29	:	-						:	-
TrMDHb30	:	-						:	-
TrMDHb31	:	-						:	-
TrMDHb32	:	-						:	-

	*      140      *	*      160      *	*      180	
TrMDHb1	: TCAAAAAATGGCCAAAGACCCAGTTCTCGTCACTGGTGCTGCAGGGCAAATTGGT			: 164
TrMDHb2	: TCAAAAAATGGCCAAAGACCCAGTTCTCGTCACTGGTGCTGCAGGGCAAATTGGT			: 162
TrMDHb3	: TCAAAAAATGGCCAAAGACCCAGTTCTCGTCACTGGTGCTGCAGGGCAAATTGGT			: 154
TrMDHb4	: TCAGGAATGGCCAAAGACCCAGTTCTCGTGTCTCGTACTGGTGCTGCAGGGCAAATTGGT			: 151
TrMDHb5	: TCAAAAAATGGCCAAAGACCCAGTTCTCGTGTCTCGTACTGGTGCTGCAGGGCAAATTGGT			: 151
TrMDHb6	: TCAGGAATGGCCAAAGACCCAGTTCTCGTGTCTCGTACTGGTGCTGCAGGGCAAATTGGT			: 144
TrMDHb7	: TCAGGAATGGCCAAAGACCCAGTTCTCGTGTCTCGTACTGGTGCTGCAGGGCAAATTGGT			: 145
TrMDHb8	: TCAGGAATGGCCAAAGACCCAGTTCTCGTGTCTCGTACTGGTGCTGCAGGGCAAATTGGT			: 144
TrMDHb9	: TCAAAAAATGGCCAAAGACCCAGTTCTCGTGTCTCGTACTGGTGCTGCAGGGCAAATTGGT			: 132
TrMDHb10	: TCAAAAAATGGCCAAAGACCCAGTTCTCGTGTCTCGTACTGGTGCTGCAGGGCAAATTGGT			: 138
TrMDHb11	: TCAAAAAATGGCCAAAGACCCAGTTCTCGTGTCTCGTACTGGTGCTGCAGGGCAAATTGGT			: 140
TrMDHb12	: TCAAAAAATGGCCAAAGACCCAGTTCTCGTGTCTCGTACTGGTGCTGCAGGGCAAATTGGT			: 141
TrMDHb13	: TCAGGAATGGCCAAAGACCCAGTTCTCGTGTCTCGTACTGGTGCTGCAGGGCAAATTGGT			: 135
TrMDHb14	: TCAAAAAATGGCCAAAGACCCAGTTCTCGTGTCTCGTACTGGTGCTGCAGGGCAAATTGGT			: 131
TrMDHb15	: TCAAAAAATGGCCAAAGACCCAGTTCTCGTGTCTCGTACTGGTGCTGCAGGGCAAATTGGT			: 139
TrMDHb16	: TCAAAAAATGGCCAAAGACCCAGTTCTCGTGTCTCGTACTGGTGCTGCAGGGCAAATTGGT			: 138
TrMDHb17	: TCAAAAAATGGCCAAAGACCCAGTTCTCGTGTCTCGTACTGGTGCTGCAGGGCAAATTGGT			: 136
TrMDHb18	: TCAAAAAATGGCCAAAGACCCAGTTCTCGTGTCTCGTACTGGTGCTGCAGGGCAAATTGGT			: 134
TrMDHb19	: TCAAAAAATGGCCAAAGACCCAGTTCTCGTGTCTCGTACTGGTGCTGCAGGGCAAATTGGT			: 130
TrMDHb20	: TCAAAAAATGGCCAAAGACCCAGTTCTCGTGTCTCGTACTGGTGCTGCAGGGCAAATTGGT			: 123
TrMDHb21	: TCAAAAAATGGCCAAAGACCCAGTTCTCGTGTCTCGTACTGGTGCTGCAGGGCAAATTGGT			: 123
TrMDHb22	: TCAAAAAATGGCCAAAGACCCAGTTCTCGTGTCTCGTACTGGTGCTGCAGGGCAAATTGGT			: 119
TrMDHb23	: T-AAAATGGCCAAAGACCCAGTTCTCGTGTCTCGTACTGGTGCTGCAGGGCAAATTGGT			: 110
TrMDHb24	: TCAAAAAATGGCCAAAGACCCAGTTCTCGTGTCTCGTACTGGTGCTGCAGGGCAAATTGGT			: 109
TrMDHb25	: TCAAAAAATGGCCAAAGACCCAGTTCTCGTGTCTCGTACTGGTGCTGCAGGGCAAATTGGT			: 106
TrMDHb26	: T-AAAATGGCCAAAGACCCAGTTCTCGTGTCTCGTACTGGTGCTGCAGGGCAAATTGGT			: 103
TrMDHb27	: T-AAAATGGCCAAAGACCCAGTTCTCGTGTCTCGTACTGGTGCTGCAGGGCAAATTGGT			: 97
TrMDHb28	: -----			:
TrMDHb29	: -----			:
TrMDHb30	: -----			:
TrMDHb31	: -----			:
TrMDHb32	: -----			:

	* 200	* 220	* 240	
TrMDHb1 :	TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC			: 224
TrMDHb2 :	TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC			: 222
TrMDHb3 :	TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC			: 214
TrMDHb4 :	TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC			: 211
TrMDHb5 :	TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC			: 211
TrMDHb6 :	TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC			: 204
TrMDHb7 :	TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC			: 205
TrMDHb8 :	TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC			: 204
TrMDHb9 :	TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC			: 192
TrMDHb10 :	TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC			: 198
TrMDHb11 :	TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC			: 200
TrMDHb12 :	TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC			: 201
TrMDHb13 :	TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC			: 195
TrMDHb14 :	TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC			: 191
TrMDHb15 :	TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC			: 199
TrMDHb16 :	TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC			: 198
TrMDHb17 :	TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC			: 196
TrMDHb18 :	TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC			: 194
TrMDHb19 :	TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC			: 190
TrMDHb20 :	TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC			: 183
TrMDHb21 :	TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC			: 183
TrMDHb22 :	TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC			: 179
TrMDHb23 :	TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC			: 170
TrMDHb24 :	TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC			: 169
TrMDHb25 :	TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC			: 166
TrMDHb26 :	TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC			: 163
TrMDHb27 :	TATGCACTTGTCCCTATGATTGCTAGGGGAGTGATGCTTGGTCCTGATCAACCTGTGATC			: 157
TrMDHb28 :	- - - - - GGGGAGTGATGCTTGGTCCTGAT- - NACCTGTGATC			: 34
TrMDHb29 :	- - - - -			: -
TrMDHb30 :	- - - - -			: -
TrMDHb31 :	- - - - -			: -
TrMDHb32 :	- - - - -			: -

	* 260 *	* 280 *	* 300 *
TrMDHb1	: CTA <sup>A</sup> CACATGCTTGTATATTCCACC <sup>G</sup> CAGCAGAGTCATTGAATGGAGTTAAGATGGAGATG		: 284
TrMDHb2	: CTA <sup>A</sup> CACATGCTTGTATATTCCACC <sup>G</sup> CAGCAGAGTCATTGAATGGAGTTAAGATGGAGTTG		: 282
TrMDHb3	: CTTCACATGCTTGTATAT <sup>C</sup> CCTCCAGCAGCAGAGTCATTGAATGGAGTTAA <sup>A</sup> ATGGAGTTG		: 274
TrMDHb4	: CTTCACATGCTTGTATAT <sup>C</sup> CCTCCAGCAGCAGAGTCATTGAATGGAGTTAA <sup>A</sup> ATGGAGTTG		: 271
TrMDHb5	: CTTCACATGCTTGTATATTCCCTCCAGCAGCAGAGTCATTGAATGGAGTTAAGATGGAGTTG		: 271
TrMDHb6	: CTTCACATGCTTGTATAT <sup>C</sup> CCTCCAGCAGCAGAGTCATTGAATGGAGTTAA <sup>A</sup> ATGGAGTTG		: 264
TrMDHb7	: CTTCACATGCTTGTATAT <sup>C</sup> CCTCCAGCAGCAGAGTCATTGAATGGAGTTAA <sup>A</sup> ATGGAGTTG		: 265
TrMDHb8	: CTTCACATGCTTGTATAT <sup>C</sup> CCTCCAGCAGCAGAGTCATTGAATGGAGTTAA <sup>A</sup> ATGGAGTTG		: 264
TrMDHb9	: CTTGACATGCTTGTATATT <sup>C</sup> T <sup>G</sup> AG <sup>N</sup> AGAGTNATTGAATGGAGCTAA <sup>A</sup> ATGGAGCTG		: 252
TrMDHb10	: CT <sup>A</sup> ACACATGCTTGTATATTCCACC <sup>G</sup> CAGCAGAGTCATTGAATGGAGTTAAGATGGAGTTG		: 258
TrMDHb11	: CTTCACATGCTTGTATATTCCCTCCAGCAGCAGAGTCATTGAATGGAGTTAAGATGGAGTTG		: 260
TrMDHb12	: CT <sup>A</sup> ACACATGCTTGTATATTCCACC <sup>G</sup> CAGCAGAGTCATTGAATGGAGTTAAGATGGAGTTG		: 261
TrMDHb13	: CTTCACATGCTTGTATAT <sup>C</sup> CCTCCAGCAGCAGAGTCATTGAATGGAGTTAA <sup>A</sup> ATGGAGTTG		: 255
TrMDHb14	: CTTCACATGCTTGTATATTCCCTCCAGCAGCAGAGTCATTGAATGGAGTTAA <sup>A</sup> ATGGAGTTG		: 251
TrMDHb15	: CT <sup>A</sup> ACACATGCTTGTATATTCCACC <sup>G</sup> CAGCAGAGTCATTGAATGGAGTTAAGATGGAGTTG		: 259
TrMDHb16	: CT <sup>A</sup> ACACATGCTTGTATATTCCACC <sup>G</sup> CAGCAGAGTCATTGAATGGAGTTAAGATGGAGTTG		: 258
TrMDHb17	: CTTCACATGCTTGTATATTCCCTCCAGCAGCAGCAGAGTCATTGAATGGAGTTAA <sup>A</sup> ATGGAGTTG		: 256
TrMDHb18	: CTTCACATGCTTGTATATTCCCTCCAGCAGCAGCAGAGTCATTGAATGGAGTTAAGATGGAGTTG		: 254
TrMDHb19	: CTTCACATGCTTGTATATTCCCTCCAGCAGCAGCAGAGTCATTGAATGGAGTTAA <sup>A</sup> ATGGAGTTG		: 250
TrMDHb20	: CTTCACATGCTTGTATATTCCCTCCAGCAGCAGCAGAGTCATTGAATGGAGTTAA <sup>A</sup> ATGGAGTTG		: 243
TrMDHb21	: CTTCACATGCTTGTATATTCCCTCCAGCAGCAGCAGAGTCATTGAATGGAGTTAAGATGGAGTTG		: 243
TrMDHb22	: CTTCACATGCTTGTATATTCCCTCCAGCAGCAGAGTCATTGAATGGAGTTAA <sup>A</sup> ATGGAGTTG		: 239
TrMDHb23	: CT <sup>A</sup> ACACATGCTTGTATATTCCACC <sup>G</sup> CAGCAGAGTCATTGAATGGAGTTAAGATGGAGTTG		: 230
TrMDHb24	: CT <sup>A</sup> ACACATGCTTGTATATTCCACC <sup>G</sup> CAGCAGAGTCATTGAATGGAGTTAAGATGGAGTTG		: 229
TrMDHb25	: CTTCACATGCTTGTATATTCC <sup>A</sup> CAGCAGCAGCAGAGTCATTGAATGGAGTTAAGATGGAGTTG		: 226
TrMDHb26	: CTTCACATGCTTGTATATTCCCTCCAGCAGCAGCAGAGTCATTGAATGGAGTTAA <sup>A</sup> ATGGAGTTG		: 223
TrMDHb27	: CTTCACATGCTTGTATATTCCCTCCAGCAGCAGCAGAGTCATTGAATGGAGTTAAGATGGAGTTG		: 217
TrMDHb28	: CTT <sup>-</sup> NCATGCTTGTATAT <sup>C</sup> CCTCCAGCAGCAGCAGAGTCATTGAATGGAGTTAA <sup>A</sup> ATGGAGTTG		: 93
TrMDHb29	: -----NTATTCC <sup>T</sup> NC <sup>N</sup> GCAGC <sup>N</sup> AGAGT-----NTTGAAATGGAGTTAAGATGGAGTTG		: 45
TrMDHb30	: -----TATTCC <sup>T</sup> CC <sup>G</sup> CAGCAGAGT-----NTTGAAATGGAGTTAAGATGGAGTTG		: 43
TrMDHb31	: -----		: -
TrMDHb32	: -----		: -

	* 320	* 340	* 360	
TrMDHb1	: G <del>N</del> GATGCTGNATTNNCACTT <del>G</del> TTAAAGG <del>N</del> G <del>A</del> G <del>C</del> TGCT	- - -	- - -	: 323
TrMDHb2	: GTCGATGCTGCATTCCACTT <del>G</del> TTAAAGGTG <del>N</del> TG <del>A</del> TGNTACAAC <del>T</del> GATG <del>A</del> TG <del>E</del> NGA <del>E</del> GN	-	-	: 342
TrMDHb3	: GTGGATGCTGCATTCCACTT <del>G</del> TTAAAGGTG <del>T</del> TGCTACAAC <del>T</del> GATG <del>T</del> TGTTGAAGCA	-	-	: 334
TrMDHb4	: GTGGATGCTGCATTCCACTT <del>G</del> TTAAAGGTG <del>T</del> TGCTACAAC <del>T</del> GATG <del>T</del> TGTTGAAGCA	-	-	: 331
TrMDHb5	: GTCGATGCTGCATTCCACTT <del>G</del> TTAAAGGTG <del>T</del> TGCTACAAC <del>T</del> GATG <del>T</del> TGTTGA <del>E</del> GC	-	-	: 331
TrMDHb6	: GTGGATGCTGCATTCCACTT <del>G</del> TTAAAGG <del>C</del> GTTGCTACAAC <del>T</del> GATG <del>T</del> TGTTGAAGCA	-	-	: 324
TrMDHb7	: GGGGATGCTGCATTCCACTT <del>G</del> TTAAAGG <del>C</del> GTTGCTACAAC <del>T</del> GATG <del>T</del> TGTTGAAGCA	-	-	: 325
TrMDHb8	: GTGGATGCTGCATTCCACTT <del>G</del> TTAAAGG <del>C</del> GTTGCTACAAC <del>T</del> GATG <del>T</del> TGTTGAAGCA	-	-	: 324
TrMDHb9	: GCGGATGCTGNATTNN <del>A</del> CTTCTTA <del>C</del> AGGGG <del>C</del> <del>E</del> G <del>C</del> GC <del>T</del> AC <del>C</del> ACTGATG <del>E</del> TG <del>C</del> <del>E</del> CAAGCA	-	-	: 312
TrMDHb10	: GTCGATGCTGCATTCCACTT <del>G</del> TTAAAGGTG <del>T</del> TGCTACAAC <del>T</del> GATG <del>T</del> TGTTGAAGCA	-	-	: 318
TrMDHb11	: GTCGATGCTGCATTCCACTT <del>G</del> TTAAAGGTG <del>T</del> TGCTACAAC <del>T</del> GATG <del>T</del> TGTTGAGGCA	-	-	: 320
TrMDHb12	: GTCGATGCTGCATTCCACTT <del>G</del> TTAAAGGTG <del>T</del> TGCTACAAC <del>T</del> GATG <del>T</del> TGTTGAGGCA	-	-	: 321
TrMDHb13	: GTGGATGCTGCATTCCACTT <del>G</del> TTAAAGG <del>C</del> GTTGCTACAAC <del>T</del> GATG <del>T</del> TGTTGAAGCA	-	-	: 315
TrMDHb14	: GTGGATGCTGCATTCCACTT <del>G</del> TTAAAGGTG <del>T</del> TGCTACAAC <del>T</del> GATG <del>T</del> TGTTGAAGCA	-	-	: 311
TrMDHb15	: GTCGATGCTGCATTCCACTT <del>G</del> TTAAAGGTG <del>T</del> TGCTACAAC <del>T</del> GATG <del>T</del> TGTTGA <del>E</del> GC	-	-	: 319
TrMDHb16	: GTCGATGCTGCATTCCACTT <del>G</del> TTAAAGGTG <del>T</del> TGCTACAAC <del>T</del> GATG <del>T</del> TGTTGAGGCA	-	-	: 318
TrMDHb17	: GTGGATGCTGCATTCCACTT <del>G</del> TTAAAGGTG <del>T</del> TGCTACAAC <del>T</del> GATG <del>T</del> TGTTGAAGCA	-	-	: 316
TrMDHb18	: GTCGATGCTGCATTCCACTT <del>G</del> TTAAAGGTG <del>T</del> TGCTACAAC <del>T</del> GATG <del>T</del> TGTTGAAGCA	-	-	: 314
TrMDHb19	: GTGGATGCTGCATTCCACTT <del>G</del> TTAAAGGTG <del>T</del> TGCTACAAC <del>T</del> GATG <del>T</del> TGTTGAAGCA	-	-	: 310
TrMDHb20	: GTGGATGCTGCATTCCACTT <del>G</del> TTAAAGGTG <del>T</del> TGCTACAAC <del>T</del> GATG <del>T</del> TGTTGAAGCA	-	-	: 303
TrMDHb21	: GTCGATGCTGCATTCCACTT <del>G</del> TTAAAGGTG <del>T</del> TGCTACAAC <del>T</del> GATG <del>T</del> TGTTGAAGCA	-	-	: 303
TrMDHb22	: GTGGATGCTGCATTCCACTT <del>G</del> TTAAAGGTG <del>T</del> TGCTACAAC <del>T</del> GATG <del>T</del> TGTTGAAGCA	-	-	: 299
TrMDHb23	: GTCGATGCTGCATTCCACTT <del>G</del> TTAAAGGTG <del>T</del> TGCTACAAC <del>T</del> GATG <del>T</del> TGTTGAGGCA	-	-	: 290
TrMDHb24	: GTCGATGCTGCATTCCACTT <del>G</del> TTAAAGGTG <del>T</del> TGCTACAAC <del>T</del> GATG <del>T</del> TGTTGAGGCA	-	-	: 289
TrMDHb25	: GTCGATGCTGCATTCCACTT <del>G</del> TTAAAGGTG <del>T</del> TGCTACAAC <del>T</del> GATG <del>T</del> TGTTGA <del>E</del> GC	-	-	: 286
TrMDHb26	: GTGGATGCTGCATTCCACTT <del>G</del> TTAAAGGTG <del>T</del> TGCTACAAC <del>T</del> GATG <del>T</del> TGTTGAAGCA	-	-	: 283
TrMDHb27	: GTCGATGCTGCATTCCACTT <del>G</del> TTAAAGGTG <del>T</del> TGCTACAAC <del>T</del> GATG <del>T</del> TGTTGA <del>E</del> GC	-	-	: 277
TrMDHb28	: GTGGATGCTGCATTCCACTT <del>G</del> TTAAAGG <del>C</del> TG <del>T</del> TGCTACAAC <del>T</del> GATG <del>T</del> TGTTGAAGCA	-	-	: 153
TrMDHb29	: GTCGATGCTGCATTCCACTT <del>G</del> TTAAAGGTG <del>T</del> TGCTACAAC <del>T</del> GATG <del>T</del> TGTTGAAGCA	-	-	: 105
TrMDHb30	: GTCGATGCTGCATTCCACTT <del>G</del> TTAAAGGTG <del>T</del> TGCTACAAC <del>T</del> GATG <del>T</del> TGTTGAAGCA	-	-	: 102
TrMDHb31	: - - -	-	-	: -
TrMDHb32	: - - -	-	-	: -

\* 380

\* 400

\* 420

TrMDHb1	:	-----	:	-
TrMDHb2	:	TNNNCTGG-----	:	350
TrMDHb3	:	TGCACTGGAGTCATAATTGCAGTCATGGTTGGATTCCAAGAAAAGAAGGTATGGAG	:	394
TrMDHb4	:	TGCACTGGAGTCATAATTGCAGTCATGGTTGGATTCCAAGAAAAGAAGGTATGGAG	:	391
TrMDHb5	:	TGCACTGGAGTCATAATTGCAGTCATGGTTGGATTCCAAGAAAAGAAGGTATGGAG	:	391
TrMDHb6	:	TGCACTGGAGTCATAATTGCAGTCATGGTTGGATTCCAAGAAAAGAAGGTATGGAG	:	384
TrMDHb7	:	TGCACTGGAGTCATAATTGCAGTCATGGTTGGATTCCAAGAAAAGAAGGTATGGAG	:	385
TrMDHb8	:	TGCACTGGAGTCATAATTGCAGTCATGGTTGGATTCCAAGAAAAGAAGGTATGGAG	:	384
TrMDHb9	:	TGCCTGGA-----CCATATNCNN-----	:	333
TrMDHb10	:	TGCACTGGAGTCATAATTGCAGTCATGGTTGGATTCCAAGAAAAGAAGGTATGGAG	:	378
TrMDHb11	:	TGCACTGGAGTCATAATTGCAGTCATGGTTGGATTCCAAGAAAAGAAGGTATGGAG	:	380
TrMDHb12	:	TGCACTGGAGTCATAATTGCAGTCATGGTTGGATTCCAAGAAAAGAAGGTATGGAG	:	381
TrMDHb13	:	TGCACTGGAGTCATAATTGCAGTCATGGTTGGATTCCAAGAAAAGAAGGTATGGAG	:	375
TrMDHb14	:	TGCACTGGAGTCATAATTGCAGTCATGGTTGGATTCCAAGAAAAGAAGGTATGGAG	:	371
TrMDHb15	:	TGCACTGGAGTCATAATTGCAGTCATGGTTGGATTCCAAGAAAAGAAGGTATGGAG	:	379
TrMDHb16	:	TGCACTGGAGTCATAATTGCAGTCATGGTTGGATTCCAAGAAAAGAAGGTATGGAG	:	378
TrMDHb17	:	TGCACTGGAGTCATAATTGCAGTCATGGTTGGATTCCAAGAAAAGAAGGTATGGAG	:	376
TrMDHb18	:	TGCACTGGAGTCATAATTGCAGTCATGGTTGGATTCCAAGAAAAGAAGGTATGGAG	:	374
TrMDHb19	:	TGCACTGGAGTCATAATTGCAGTCATGGTTGGATTCCAAGAAAAGAAGGTATGGAG	:	370
TrMDHb20	:	TGCACTGGAGTCATAATTGCAGTCATGGTTGGATTCCAAGAAAAGAAGGTATGGAG	:	363
TrMDHb21	:	TGCACTGGAGTCATAATTGCAGTCATGGTTGGATTCCAAGAAAAGAAGGTATGGAG	:	363
TrMDHb22	:	TGCACTGGAGTCATAATTGCAGTCATGGTTGGATTCCAAGAAAAGAAGGTATGGAG	:	359
TrMDHb23	:	TGCACTGGAGTCATAATTGCAGTCATGGTTGGATTCCAAGAAAAGAAGGTATGGAG	:	350
TrMDHb24	:	TGCACTGGAGTCATAATTGCAGTCATGGTTGGATTCCAAGAAAAGAAGGTATGGAG	:	349
TrMDHb25	:	TGCACTGGAGTCATAATTGCAGTCATGGTTGGATTCCAAGAAAAGAAGGTATGGAG	:	346
TrMDHb26	:	TGCACTGGAGTCATAATTGCAGTCATGGTTGGATTCCAAGAAAAGAAGGTATGGAG	:	343
TrMDHb27	:	TGCACTGGAGTCATAATTGCAGTCATGGTTGGATTCCAAGAAAAGAAGGTATGGAG	:	337
TrMDHb28	:	TGCACTGGAGTCATAATTGCAGTCATGGTTGGATTCCAAGAAAAGAAGGTATGGAG	:	213
TrMDHb29	:	TGCACTGGAGTCATAATTGCAGTCATGGTTGGATTCCAAGAAAAGAAGGTATGGAG	:	165
TrMDHb30	:	TGCACTGGAGTCATAATTGCAGTCATGGTTGGATTCCAAGAAAAGAAGGTATGGAG	:	162
TrMDHb31	:	-----	GGAG	: 4
TrMDHb32	:	-----	NNNN	: 4

	* 440	* 460	* 480	
TrMDHb1	:	-	-	
TrMDHb2	:	-	-	
TrMDHb3	: AGGAAGGATGTGATGACTAAGAACGTCTCTATTACAAGTCCCAGGCCCTTGAA			: 454
TrMDHb4	: AGGAAGGATGTGATGACTAAGAACGTCTCTATTACAAGTCCCAGGCCCTTGAA			: 451
TrMDHb5	: AGGAAGGATGTGATGACTAAGAACGTCTCTATTACAAGTCCCAGGCCCTTGAA			: 451
TrMDHb6	: AGGAAGGATGTGATGACTAAGAACGTCTCTATTACAAGTCCCAGGCCCTTGAA			: 444
TrMDHb7	: AGGAAGGATGTGATGACTAAGAACGTCTCTATTACAAGTCCCAGGCCCTTGAA			: 445
TrMDHb8	: AGGAAGGATGTGATGACTAAGAACGTCTCTATTACAAGTCCCAGGCCCTTGAA			: 444
TrMDHb9	:	-	-	
TrMDHb10	: AGGAAGGATGTGATGACTAAGAACGTCTCTATTACAAGTCCCAGGCCCTTGAA			: 438
TrMDHb11	: AGGAAGGATGTGATGACTAAGAACGTCTCTATTACAAGTCCCAGGCCCTTGAA			: 440
TrMDHb12	: AGGAAGGATGTGATGACTAAGAACGTCTCTATTACAAGTCCCAGGCCCTTGAA			: 441
TrMDHb13	: AGGAAGGATGTGATGACTAAGAACGTCTCTATTACAAGTCCCAGGCCCTTGAA			: 435
TrMDHb14	: AGGAAGGATGTGATGACTAAGAACGTCTCTATTACAAGTCCCAGGCCCTTGAA			: 431
TrMDHb15	: AGGAAGGATGTGATGACTAAGAACGTCTCTATTACAAGTCCCAGGCCCTTGAA			: 439
TrMDHb16	: AGGAAGGATGTGATGACTAAGAACGTCTCTATTACAAGTCCCAGGCCCTTGAA			: 438
TrMDHb17	: AGGAAGGATGTGATGACTAAGAACGTCTCTATTACAAGTCCCAGGCCCTTGAA			: 436
TrMDHb18	: AGGAAGGATGTGATGACTAAGAACGTCTCTATTACAAGTCCCAGGCCCTTGAA			: 434
TrMDHb19	: AGGAAGGATGTGATGACTAAGAACGTCTCTATTACAAGTCCCAGGCCCTTGAA			: 430
TrMDHb20	: AGGAAGGATGTGATGACTAAGAACGTCTCTATTACAAGTCCCAGGCCCTTGAA			: 423
TrMDHb21	: AGGAAGGATGTGATGACTAAGAACGTCTCTATTACAAGTCCCAGGCCCTTGAA			: 423
TrMDHb22	: AGGAAGGATGTGATGACTAAGAACGTCTCTATTACAAGTCCCAGGCCCTTGAA			: 419
TrMDHb23	: AGGAAGGATGTGATGACTAAGAACGTCTCTATTACAAGTCCCAGGCCCTTGAA			: 410
TrMDHb24	: AGGAAGGATGTGATGACTAAGAACGTCTCTATTACAAGTCCCAGGCCCTTGAA			: 409
TrMDHb25	: AGGAAGGATGTGATGACTAAGAACGTCTCTATTACAAGTCCCAGGCCCTTGAA			: 406
TrMDHb26	: AGGAAGGATGTGATGACTAAGAACGTCTCTATTACAAGTCCCAGGCCCTTGAA			: 403
TrMDHb27	: AGGAAGGATGTGATGACTAAGAACGTCTCTATTACAAGTCCCAGGCCCTTGAA			: 397
TrMDHb28	: AGGAAGGATGTGATGACTAAGAACGTCTCTATTACAAGTCCCAGGCCCTTGAA			: 273
TrMDHb29	: AGGAAGGATGTGATGACTAAGAACGTCTCTATTACAAGTCCCAGGCCCTTGAA			: 225
TrMDHb30	: AGGAAGGATGTGATGACTAAGAACGTCTCTATTACAAGTCCCAGGCCCTTGAA			: 222
TrMDHb31	: AGGAAGGATGTGATGACTAAGAACGTCTCTATTACAAGTCCCAGGCCCTTGAA			: 64
TrMDHb32	: NNGNANGNNGTGTGACTAACACGTCTCTATTACAAGTCCCAGGCCCTTGAA			: 64

	* 500	* 520	* 540	
TrMDHb1	:	-	-	:
TrMDHb2	:	-	-	:
TrMDHb3	:	AAGCATGCTGCCA <b>ACTGCAAGGTTTGTTATTGCTAACCCAGC</b> AAA <b>TACCAATGCA</b>		: 514
TrMDHb4	:	AAGCATGCTGCCA <b>ACTGCAAGGTTTGTTATTGCTAACCCAGC</b> AAA <b>TACCAATGCA</b>		: 511
TrMDHb5	:	AAGCATGCTGCCA <b>ACTGCAAGGNTTGTTGNTGCTAACCCAN</b> C <b>AACACCAATGCA</b>		: 510
TrMDHb6	:	AAGCATGCTGCCA <b>ACTGCAAGGTTTGTTATTGCTAACCCAGC</b> AAA <b>TACCAATGCA</b>		: 504
TrMDHb7	:	AAGCATGCTGCCA <b>ACTGCAAGGTTTGTTATTGCTAACCCAGC</b> AAA <b>TACCAATGCA</b>		: 505
TrMDHb8	:	AAGCATGCTGCCA <b>ACTGCAAGGTTTGTTATTGCTAACCCAGC</b> AAA <b>TACCAATGCA</b>		: 504
TrMDHb9	:	-	-	:
TrMDHb10	:	AAGCATGCTGCCA <b>ACTGCAAGGTTTGTTGTTGCTAACCCAGC</b> AAA <b>ACACCAATGCA</b>		: 498
TrMDHb11	:	AAGCATGCTGCCA <b>ACTGCAAGGTTTGTTGTTGCTAACCCAGC</b> AAA <b>ACACCAATGCA</b>		: 499
TrMDHb12	:	AAGCATGCTGCCA <b>ACTGCAAGGTTTGTTGTTGCTAACCCAGC</b> AAA <b>ACACCAATGCA</b>		: 501
TrMDHb13	:	AAGCATGCTGCCA <b>ACTGCAAGGTTTGTTGTTGCTAACCCAGC</b> AAA <b>ACACCAATGCA</b>		: 495
TrMDHb14	:	AAGCATGCTGCCA <b>ACTGCAAGGTTTGTTG</b>		: 462
TrMDHb15	:	AAGCATGCTGCCA <b>ACTGCAAGGTTTGTTGTTGCTAACCCAGC</b> AAA <b>ACACCAATGCA</b>		: 499
TrMDHb16	:	AAGCATGCTGCCA <b>ACTGCAAGGTTTGTTGTTGCTAACCCAGC</b> AAA <b>ACACCAATGCA</b>		: 498
TrMDHb17	:	AAGCATGCTGCCA <b>ACTGCAAGGNTTGTTGTTGCTAACCCAN</b> C <b>AACACCAATGCA</b>		: 496
TrMDHb18	:	AAGCATGCTGCCA <b>ACTGCAAGGTTTGTTGTTGCTAACCCAGC</b> AAA <b>ACACCAATGCA</b>		: 493
TrMDHb19	:	AAGCATGCTGCCA <b>ACTGCAAGGTTTGTTGTTGCTAACCCAGC</b> AAA <b>ACACCAATGCA</b>		: 490
TrMDHb20	:	AAGCATGCTGCCA <b>ACTGCAAGGTTTGTTGTTGCTAACCCAGC</b> AAA <b>ACACCAATGCA</b>		: 433
TrMDHb21	:	AAGCATGCTGCCA <b>ACTGCAAGGTTTGTTGTTGCTAACCCAGC</b> AAA <b>ACACCAATGCA</b>		: 483
TrMDHb22	:	AAGCATGCTGCCA <b>ACTGCAAGGTTTGTTGTTGCTAACCCAGC</b> AAA <b>ACACCAATGCA</b>		: 479
TrMDHb23	:	AAGCATGCTGCCA <b>ACTGCAAGGTTTGTTGTTGCTAACCCAGC</b> AAA <b>ACACCAATGCA</b>		: 470
TrMDHb24	:	AAGCATGCTGCCA <b>ACTGCAAGGTTTGTTGTTGCTAACCCAGC</b> AAA <b>ACACCAATGCA</b>		: 469
TrMDHb25	:	AAGCATGCTGCCA <b>ACTGCAAGGTTTGTTGTTGCTAACCCAGC</b> AAA <b>ACACCAATGCA</b>		: 466
TrMDHb26	:	AAGCATGCTGCCA <b>ACTGCAAGGTTTGTTGTTGCTAACCCAGC</b> AAA <b>ACACCAATGCA</b>		: 463
TrMDHb27	:	AAGCATGCTGCCA <b>ACTGCAAGGTTTGTTGTTGCTAACCCAGC</b> AAA <b>ACACCAATGCA</b>		: 457
TrMDHb28	:	AAGCATGCTGCCA <b>ACTGCAAGGTTTGTTGTTGCTAACCCAGC</b> AAA <b>ACACCAATGCA</b>		: 333
TrMDHb29	:	AAGCATGCTGCCA <b>ACTGCAAGGTTTGTTGTTGCTAACCCAGC</b> AAA <b>ACACCAATGCA</b>		: 285
TrMDHb30	:	AAGCATGCTGCCA <b>ACTGCAAGGTTTGTTGTTGCTAACCCAGC</b> AAA <b>ACACCAATGCA</b>		: 282
TrMDHb31	:	AAGCATGCTGCCA <b>ACTGCAAGGTTTGTTGTTGCTAACCCAGC</b> AAA <b>ACACCAATGCA</b>		: 124
TrMDHb32	:	AAGCATGCTGCCA <b>ACTGCAAGGTTTGTTGTTGCTAACCCAGC</b> AAA <b>ACACCAATGCA</b>		: 124

\* 560 \* 580 \* 600

TrMDHb1	:	- - - - -	:	-
TrMDHb2	:	- - - - -	:	-
TrMDHb3	:	TTGATCTTGAAGGAGTTGCTCCATCTATTCCAGAGAAAAACATTCAGCTTGACTAGA	:	574
TrMDHb4	:	TTGATCTTGAAGGAGTTGCTCCATCTATTCCAGAGAAAAACATTCAGCTTGACTAGA	:	571
TrMDHb5	:	TTGATCTTGNAGGAATCNGCT-----	:	531
TrMDHb6	:	TTGATCTTGAAGGAGTTGCTCCATCTATTCCAGAGAAAAACATTCAGCTTGACTAGA	:	564
TrMDHb7	:	TTGATCTTGAAGGAGTTGCTCCATCTATTCCAGAGAAAAACATTCAGCTTGACTAGA	:	565
TrMDHb8	:	TTGATCTTGAAGGAGTTGCTCCATCTATTCCAGAGAAAAACATTCAGCTTGACTAGA	:	564
TrMDHb9	:	- - - - -	:	-
TrMDHb10	:	TTGATCTTGAAGGAAATTGCTCCATCTATTCCAGAGAAAAACATTCCTGTGTTGACTAGA	:	558
TrMDHb11	:	TTGATCTTGAAGGAAATTGCTCCATCTATTCCAGAGAAAAACATTCCTGTGTTGACTAGA	:	559
TrMDHb12	:	TTGATCTTGAAGGAAATTGCTCCATCTATTCCAGAGAAAAACATTCCTGTGTTGACTAGA	:	561
TrMDHb13	:	TTGATCTTGAAGGAGTTGCTCCATCTATTCCAGAGAAAAACATTCAGCTTGACTAGA	:	555
TrMDHb14	:	- - - - -	:	-
TrMDHb15	:	TTGATCTTGAAGGAAATTGCTCCATCTATTCCAGAGAAAAACATTCCTGTGTTGACTAGA	:	559
TrMDHb16	:	TTGATCTTGAAGGAAATTGCTCCATCTATTCCAGAGAAAAACATTCCTGTGTTGACTAGA	:	558
TrMDHb17	:	TTGATCTTGAAGGAGTTGCTCCATCTATTCCAGAGAAAAACATTCANNTTG-----	:	550
TrMDHb18	:	TTGATCTTGAAGGAAATTGCTCCATCTATTCCAGAGAAAAACATTCCTGTGTTGACTAGA	:	553
TrMDHb19	:	TTGATCTTGAAGGAGTTGCTCCATCTATTCCAGAGAAAAACATTCAGCTTGACTAGA	:	550
TrMDHb20	:	- - - - -	:	-
TrMDHb21	:	TTGATCTTGAAGGAAATTGCTCCATCTATTCCAGAGAAAAACATTCCTGTGTTGACTAGA	:	543
TrMDHb22	:	TTGATCTTGAAGGAGTTGCTCCATCTATTCCAGAGAAAAACATTCAGCTTGACTAGA	:	539
TrMDHb23	:	TTGATCTTGAAGGAAATTGCTCCATCTATTCCAGAGAAAAACATTCCTGTGTTGACTAGA	:	530
TrMDHb24	:	TTGATCTTGAAGGAAATTGCTCCATCTATTCCAGAGAAAAACATTCCTGTGTTGACTAGA	:	529
TrMDHb25	:	TTGATCTTGAAGGAAATTGCTCCATCTATTCCAGAGAAAAACATTCCTGTGTTGACTAGA	:	526
TrMDHb26	:	TTGATCTTGAAGGAGTTGCTCCATCTATTCCAGAGAAAAACATTCAGCTTGACTAGA	:	523
TrMDHb27	:	TTGATCTTGAAGGAAATTGCTCCATCTATTCCAGAGAAAAACATTCAGCTTGACTAGA	:	517
TrMDHb28	:	TTGATCTTGAAGGAGTTGCTCCATCTATTCCAGAGAAAAACATTCAGCTTGACTAGA	:	393
TrMDHb29	:	TTGATCTTGAAGGAAATTGCTCCATCTATTCCAGAGAAAAACATTCCTGTGTTGACTAGA	:	345
TrMDHb30	:	TTGATCTTGAAGGAAATTGCTCCATCTATTCCAGAGAAAAACATTCCTGTGTTGACTAGA	:	342
TrMDHb31	:	TTGATCTTGAAGGAAATTGCTCCATCTATTCCAGAGAAAAACATTCCTGTGTTGACTAGA	:	184
TrMDHb32	:	TTGATCTTGAAGGAAATTGCTCCATCTATTCCAGAGAAAAACATTCCTGTGTTGACTAGA	:	184

	*      620	*      640	*      660
TrMDHb1	: -----		: -----
TrMDHb2	: -----		: -----
TrMDHb3	: CTTGATCACAA-----		: 585
TrMDHb4	: CTTGATCACACAGGGCATTGG-----		: 593
TrMDHb5	: -----		: -----
TrMDHb6	: CTTGATCAC-----		: 573
TrMDHb7	: CTTGATCACACAGGGCATTGGGCCAAATTTCTGAAAG-----		: 603
TrMDHb8	: CTTGATCACACAGGGCATTGGGCCAAATTTCT-----		: 597
TrMDHb9	: -----		: -----
TrMDHb10	: CTTGATCAC-----		: 567
TrMDHb11	: CTTGATCAC-----		: 569
TrMDHb12	: CTTGATCACACAGGGCATTGGGCCAAATTT-----		: 592
TrMDHb13	: CTTGATCACACAGGGCATTGGGCCAAATT-----		: 585
TrMDHb14	: -----		: -----
TrMDHb15	: CTTGATCACACACAG-----		: 573
TrMDHb16	: CTTGATCACACACAGGGCATTGGGCCAAATTTCTGAAAGATTGAAT-----		: 603
TrMDHb17	: -----		: -----
TrMDHb18	: CTTGATCACACACAGGGCATTGGGCCAAATTTCTGAAAG-----		: 591
TrMDHb19	: CTTGATCACACACAGGGCATTG-----		: 571
TrMDHb20	: -----		: -----
TrMDHb21	: CTTGATCACACACAGGGCATTGGGCCAAATTTCTGAAAGATTG-----		: 585
TrMDHb22	: CTTGATCACACACAGGGCATTGGGCCAAATTTCTGAAAGATTGAATATTCAGTTCTGAT-----		: 599
TrMDHb23	: CTTGATCACACACAGGGCATTGGGCCAAATTTCTGAAAG-----		: 568
TrMDHb24	: CTTGATCACACACAGGGCATTGGGCCAAAT-----		: 558
TrMDHb25	: CTTGATCACACACAGGGCATTGGGCCAAATTTCTGAAAGATTGAATGTTCAGTTCTGAT-----		: 586
TrMDHb26	: CTTGATCACACACAGGGCATTGGGCCAAATTTCTGAAAGATTGAATATTCAGTTCTGAT-----		: 583
TrMDHb27	: CTTGATCACACACAGGGCATTGGGCCAAATTTCTGAAAGATTGAATGTTCAGTTTC-----		: 573
TrMDHb28	: CTTGATCACACACAGGGCATTGGGCCAAATTTCTGAAAGATTGAATATTCAGTTCTGAT-----		: 453
TrMDHb29	: CTTGATCACACACAGGGCATTGNGCCAAATTTCTGAAAGATTGAATGTCCAGTTCTGAT-----		: 405
TrMDHb30	: CTTGATCACACACAGGGCATTGGGCCAAATTTCTGAAAGATTGAATGTTCAGTTCTGAT-----		: 402
TrMDHb31	: CTTGATCACACACAGGGCATTGGGCCAAATTTCTGAAAGATTGAATGTTCAGTTCTGAT-----		: 244
TrMDHb32	: CTTGATCACACACAGGGCATTGGGCCAAATTTCTGAAAGATTGAATGTTCAGTTCTGAT-----		: 244

	*	680	*	700	*	720	
TrMDHb1	:	- - -		- - -		- - -	:
TrMDHb2	:	- - -		- - -		- - -	:
TrMDHb3	:	- - -		- - -		- - -	:
TrMDHb4	:	- - -		- - -		- - -	:
TrMDHb5	:	- - -		- - -		- - -	:
TrMDHb6	:	- - -		- - -		- - -	:
TrMDHb7	:	- - -		- - -		- - -	:
TrMDHb8	:	- - -		- - -		- - -	:
TrMDHb9	:	- - -		- - -		- - -	:
TrMDHb10	:	- - -		- - -		- - -	:
TrMDHb11	:	- - -		- - -		- - -	:
TrMDHb12	:	- - -		- - -		- - -	:
TrMDHb13	:	- - -		- - -		- - -	:
TrMDHb14	:	- - -		- - -		- - -	:
TrMDHb15	:	- - -		- - -		- - -	:
TrMDHb16	:	- - -		- - -		- - -	:
TrMDHb17	:	- - -		- - -		- - -	:
TrMDHb18	:	- - -		- - -		- - -	:
TrMDHb19	:	- - -		- - -		- - -	:
TrMDHb20	:	- - -		- - -		- - -	:
TrMDHb21	:	- - -		- - -		- - -	:
TrMDHb22	:	<b>GTAAAGAATGT</b>		- - -		- - -	<b>610</b>
TrMDHb23	:	- - -		- - -		- - -	:
TrMDHb24	:	- - -		- - -		- - -	:
TrMDHb25	:	<b>GTAAAGAATGTCATTATCTGGGTAATCATTCAACTCAGTATCC</b>	<b>T</b>	<b>GATGTCACC</b>	<b>CAT</b>	- - -	<b>646</b>
TrMDHb26	:	- - -		- - -		- - -	:
TrMDHb27	:	- - -		- - -		- - -	:
TrMDHb28	:	<b>GTAAAGAATGTCATTATCTGGGTAATCATTCAACTCAGTATCC</b>	<b>T</b>	<b>GATGTCACC</b>	<b>CAT</b>	- - -	<b>513</b>
TrMDHb29	:	<b>GTAAAGAATGTCATTATCTGG</b>	<b>N</b>	<b>GTAATCATTCAACTCAGG</b>	<b>GATCC</b>	<b>T</b>	<b>465</b>
TrMDHb30	:	<b>GTAAAGAATGTCATTATCTGGGTAATCATTCAACTCAGTATCC</b>	<b>T</b>	<b>GATGTCACC</b>	<b>CAT</b>	- - -	<b>462</b>
TrMDHb31	:	<b>GTAAAGAATGTCATTATCTGGGTAATCATTCAACTCAGTATCC</b>	<b>T</b>	<b>GATGTCACC</b>	<b>CAT</b>	- - -	<b>304</b>
TrMDHb32	:	<b>GTAAAGAATGTCATTATCTGGGTAATCATTCAACTCAGTATCC</b>	<b>T</b>	<b>GATGTCACC</b>	<b>CAT</b>	- - -	<b>304</b>

	*	740	*	760	*	780	
TrMDHb1	:	-	-	-	-	-	-
TrMDHb2	:	-	-	-	-	-	-
TrMDHb3	:	-	-	-	-	-	-
TrMDHb4	:	-	-	-	-	-	-
TrMDHb5	:	-	-	-	-	-	-
TrMDHb6	:	-	-	-	-	-	-
TrMDHb7	:	-	-	-	-	-	-
TrMDHb8	:	-	-	-	-	-	-
TrMDHb9	:	-	-	-	-	-	-
TrMDHb10	:	-	-	-	-	-	-
TrMDHb11	:	-	-	-	-	-	-
TrMDHb12	:	-	-	-	-	-	-
TrMDHb13	:	-	-	-	-	-	-
TrMDHb14	:	-	-	-	-	-	-
TrMDHb15	:	-	-	-	-	-	-
TrMDHb16	:	-	-	-	-	-	-
TrMDHb17	:	-	-	-	-	-	-
TrMDHb18	:	-	-	-	-	-	-
TrMDHb19	:	-	-	-	-	-	-
TrMDHb20	:	-	-	-	-	-	-
TrMDHb21	:	-	-	-	-	-	-
TrMDHb22	:	-	-	-	-	-	-
TrMDHb23	:	-	-	-	-	-	-
TrMDHb24	:	-	-	-	-	-	-
TrMDHb25	:	GCAACTGTTAACACCCCCGCTGGGGAGAAGCCTGTCCGTGAGCTTGT <del>TCTGATGACGCC</del>					706
TrMDHb26	:	-	-	-	-	-	-
TrMDHb27	:	-	-	-	-	-	-
TrMDHb28	:	GCAACTGTTAACACCCCCGCTGGGGAGAAGCCTGTCCGTGA <del>ACTTGTTT</del>					562
TrMDHb29	:	GCAACTGTTAACACCC <del>N</del> CCTGNNGAGAAGCCTG <del>N</del> CCGTGAGCT <del>N</del> GTTTC					515
TrMDHb30	:	GCAACTGTTAACACCCCCGCTGGGGAGAAGCCTGTCCGTGAGCTTGT <del>TTCTGATGACGCC</del>					522
TrMDHb31	:	GCAACTGTTAACACCCCCGCTGGGGAGAAGCCTGTCCGTGAGCTTGT <del>TTCTGATGACGCC</del>					364
TrMDHb32	:	GCAACTGTTAACACCCCCGCTGGGGAGAAGCCTGTCCGTGAGCTTGT <del>TTCTGATGACGCC</del>					364

	*	800	*	820	*	840
TrMDHb1	:	-	-	-	-	-
TrMDHb2	:	-	-	-	-	-
TrMDHb3	:	-	-	-	-	-
TrMDHb4	:	-	-	-	-	-
TrMDHb5	:	-	-	-	-	-
TrMDHb6	:	-	-	-	-	-
TrMDHb7	:	-	-	-	-	-
TrMDHb8	:	-	-	-	-	-
TrMDHb9	:	-	-	-	-	-
TrMDHb10	:	-	-	-	-	-
TrMDHb11	:	-	-	-	-	-
TrMDHb12	:	-	-	-	-	-
TrMDHb13	:	-	-	-	-	-
TrMDHb14	:	-	-	-	-	-
TrMDHb15	:	-	-	-	-	-
TrMDHb16	:	-	-	-	-	-
TrMDHb17	:	-	-	-	-	-
TrMDHb18	:	-	-	-	-	-
TrMDHb19	:	-	-	-	-	-
TrMDHb20	:	-	-	-	-	-
TrMDHb21	:	-	-	-	-	-
TrMDHb22	:	-	-	-	-	-
TrMDHb23	:	-	-	-	-	-
TrMDHb24	:	-	-	-	-	-
TrMDHb25	:	TGGTTGAATGGAGAATTCA TACATATCTACCGTTCAACAACGTGGTGCTG	752			
TrMDHb26	:	-	-	-	-	-
TrMDHb27	:	-	-	-	-	-
TrMDHb28	:	-	-	-	-	-
TrMDHb29	:	-	-	-	-	-
TrMDHb30	:	TGGTTGAATGGAGAATTCA TACATATCTACCGTTCAACAACGTGGTGCTG	582			
TrMDHb31	:	TGGTTGAATGGAGAATTCA TACATATCTACCGTTCAACAACGTGGTGCTG	424			
TrMDHb32	:	TGGTTGAATGGAGAATTCA TACATATCTACCGTTCAACAACGTGGTGCTG	424			

	*	860	*	880	*	900
TrMDHb1	:	-	-	-	-	-
TrMDHb2	:	-	-	-	-	-
TrMDHb3	:	-	-	-	-	-
TrMDHb4	:	-	-	-	-	-
TrMDHb5	:	-	-	-	-	-
TrMDHb6	:	-	-	-	-	-
TrMDHb7	:	-	-	-	-	-
TrMDHb8	:	-	-	-	-	-
TrMDHb9	:	-	-	-	-	-
TrMDHb10	:	-	-	-	-	-
TrMDHb11	:	-	-	-	-	-
TrMDHb12	:	-	-	-	-	-
TrMDHb13	:	-	-	-	-	-
TrMDHb14	:	-	-	-	-	-
TrMDHb15	:	-	-	-	-	-
TrMDHb16	:	-	-	-	-	-
TrMDHb17	:	-	-	-	-	-
TrMDHb18	:	-	-	-	-	-
TrMDHb19	:	-	-	-	-	-
TrMDHb20	:	-	-	-	-	-
TrMDHb21	:	-	-	-	-	-
TrMDHb22	:	-	-	-	-	-
TrMDHb23	:	-	-	-	-	-
TrMDHb24	:	-	-	-	-	-
TrMDHb25	:	-	-	-	-	-
TrMDHb26	:	-	-	-	-	-
TrMDHb27	:	-	-	-	-	-
TrMDHb28	:	-	-	-	-	-
TrMDHb29	:	-	-	-	-	-
TrMDHb30	:	AGAAAGCTTCAAGTG	-	-	-	-
TrMDHb31	:	AGAAAGCTTCAAGCGCACTATCCGCTGCTAGCGCTGCTTCGACCAATTCGCGATTGG	-	-	-	598
TrMDHb32	:	AGAAAGCTTCAAGCGCACTATCCGCTGCTAGCGCTGCTTCGACCAATTCGCGATTGG	-	-	-	484
						484

	*	920	*	940	*	960
TrMDHb1	:	-	-	-	-	-
TrMDHb2	:	-	-	-	-	-
TrMDHb3	:	-	-	-	-	-
TrMDHb4	:	-	-	-	-	-
TrMDHb5	:	-	-	-	-	-
TrMDHb6	:	-	-	-	-	-
TrMDHb7	:	-	-	-	-	-
TrMDHb8	:	-	-	-	-	-
TrMDHb9	:	-	-	-	-	-
TrMDHb10	:	-	-	-	-	-
TrMDHb11	:	-	-	-	-	-
TrMDHb12	:	-	-	-	-	-
TrMDHb13	:	-	-	-	-	-
TrMDHb14	:	-	-	-	-	-
TrMDHb15	:	-	-	-	-	-
TrMDHb16	:	-	-	-	-	-
TrMDHb17	:	-	-	-	-	-
TrMDHb18	:	-	-	-	-	-
TrMDHb19	:	-	-	-	-	-
TrMDHb20	:	-	-	-	-	-
TrMDHb21	:	-	-	-	-	-
TrMDHb22	:	-	-	-	-	-
TrMDHb23	:	-	-	-	-	-
TrMDHb24	:	-	-	-	-	-
TrMDHb25	:	-	-	-	-	-
TrMDHb26	:	-	-	-	-	-
TrMDHb27	:	-	-	-	-	-
TrMDHb28	:	-	-	-	-	-
TrMDHb29	:	-	-	-	-	-
TrMDHb30	:	-	-	-	-	-
TrMDHb31	:	GTTCTTGGAACTCCCCAGGGCACCTTCGTTCAATGGGAGTGTATTCTGATGGTTCTTAC			: 544	
TrMDHb32	:	GTTCTTGGAACTCCCCAGGGCACCTTCGTTCAATGGGAGTGTATTCTGATGGTTCTTAC			: 544	

	*	980	*	1000	*	1020
TrMDHb1	:	-	-	-	-	-
TrMDHb2	:	-	-	-	-	-
TrMDHb3	:	-	-	-	-	-
TrMDHb4	:	-	-	-	-	-
TrMDHb5	:	-	-	-	-	-
TrMDHb6	:	-	-	-	-	-
TrMDHb7	:	-	-	-	-	-
TrMDHb8	:	-	-	-	-	-
TrMDHb9	:	-	-	-	-	-
TrMDHb10	:	-	-	-	-	-
TrMDHb11	:	-	-	-	-	-
TrMDHb12	:	-	-	-	-	-
TrMDHb13	:	-	-	-	-	-
TrMDHb14	:	-	-	-	-	-
TrMDHb15	:	-	-	-	-	-
TrMDHb16	:	-	-	-	-	-
TrMDHb17	:	-	-	-	-	-
TrMDHb18	:	-	-	-	-	-
TrMDHb19	:	-	-	-	-	-
TrMDHb20	:	-	-	-	-	-
TrMDHb21	:	-	-	-	-	-
TrMDHb22	:	-	-	-	-	-
TrMDHb23	:	-	-	-	-	-
TrMDHb24	:	-	-	-	-	-
TrMDHb25	:	-	-	-	-	-
TrMDHb26	:	-	-	-	-	-
TrMDHb27	:	-	-	-	-	-
TrMDHb28	:	-	-	-	-	-
TrMDHb29	:	-	-	-	-	-
TrMDHb30	:	-	-	-	-	-
TrMDHb31	:	AACGTACCAGCTGGACTCATCTATTCA	TTCCCTGTCACC	ACTGCTA	ATGGGGAA	603
TrMDHb32	:	AACGTACCAGCTGGACTCATCTATTCA	TTCCCTGTCACC	ACTGCTA	ATGGGGAA	604

	*	1040	*	1060	*	1080
TrMDHb1	:	-	-	-	-	-
TrMDHb2	:	-	-	-	-	-
TrMDHb3	:	-	-	-	-	-
TrMDHb4	:	-	-	-	-	-
TrMDHb5	:	-	-	-	-	-
TrMDHb6	:	-	-	-	-	-
TrMDHb7	:	-	-	-	-	-
TrMDHb8	:	-	-	-	-	-
TrMDHb9	:	-	-	-	-	-
TrMDHb10	:	-	-	-	-	-
TrMDHb11	:	-	-	-	-	-
TrMDHb12	:	-	-	-	-	-
TrMDHb13	:	-	-	-	-	-
TrMDHb14	:	-	-	-	-	-
TrMDHb15	:	-	-	-	-	-
TrMDHb16	:	-	-	-	-	-
TrMDHb17	:	-	-	-	-	-
TrMDHb18	:	-	-	-	-	-
TrMDHb19	:	-	-	-	-	-
TrMDHb20	:	-	-	-	-	-
TrMDHb21	:	-	-	-	-	-
TrMDHb22	:	-	-	-	-	-
TrMDHb23	:	-	-	-	-	-
TrMDHb24	:	-	-	-	-	-
TrMDHb25	:	-	-	-	-	-
TrMDHb26	:	-	-	-	-	-
TrMDHb27	:	-	-	-	-	-
TrMDHb28	:	-	-	-	-	-
TrMDHb29	:	-	-	-	-	-
TrMDHb30	:	-	-	-	-	-
TrMDHb31	:	-	-	-	-	-
TrMDHb32	:	ATTGTTCAAGGACTTCAATTGACCGAGTTCTAAGGAAGAAGTTGGACTTGACAGCTGAA	:	664		

\* 1100 \*

TrMDHb1 : ----- : -  
TrMDHb2 : ----- : -  
TrMDHb3 : ----- : -  
TrMDHb4 : ----- : -  
TrMDHb5 : ----- : -  
TrMDHb6 : ----- : -  
TrMDHb7 : ----- : -  
TrMDHb8 : ----- : -  
TrMDHb9 : ----- : -  
TrMDHb10 : ----- : -  
TrMDHb11 : ----- : -  
TrMDHb12 : ----- : -  
TrMDHb13 : ----- : -  
TrMDHb14 : ----- : -  
TrMDHb15 : ----- : -  
TrMDHb16 : ----- : -  
TrMDHb17 : ----- : -  
TrMDHb18 : ----- : -  
TrMDHb19 : ----- : -  
TrMDHb20 : ----- : -  
TrMDHb21 : ----- : -  
TrMDHb22 : ----- : -  
TrMDHb23 : ----- : -  
TrMDHb24 : ----- : -  
TrMDHb25 : ----- : -  
TrMDHb26 : ----- : -  
TrMDHb27 : ----- : -  
TrMDHb28 : ----- : -  
TrMDHb29 : ----- : -  
TrMDHb30 : ----- : -  
TrMDHb31 : ----- : -  
TrMDHb32 : GAGTTATCCGAGGGAAAAGAGTTGGCATACT : 695

Figure 61 Consensus contig nucleotide sequence of TrMDHc

\* 20 \* 40 \* 60  
TrMDHc : AAAGNGAATTGGAATATA CGACACTCCATTCCATACTTCCATTCCNTACTTGCTTC : 60

\* 80 \* 100 \* 120  
TrMDHc : GCTCTCTCTCTTTATTCTCGAAAAGCTTTTCAGCCAACAACGGAGAGAATTATGAGG : 120

\* 140 \* 160 \* 180  
TrMDHc : CCGTCGATGCTCAGATCCGTCCAATCAGCCGTCTCCCGCGCCTCTCACCTAACCCGC : 180

\* 200 \* 220 \* 240  
TrMDHc : CGTGGCTATGCTACCGAACCAAGAGTTCCAGAACGCAAGGTGGCCATTCTCGCGCTGCCGGC : 240

\* 260 \* 280 \* 300  
TrMDHc : GGGATCGGCCAGCCTCTCTCTCTCATGAAGCTCAACCCTCTCGTTCAACCCTATCT : 300

\* 320 \* 340 \* 360  
TrMDHc : CTTTATGATATTGCTGGAACCCCTGGTGTGCCGCTGATGTCAGCCACATCAACTCCAGA : 360

\* 380 \* 400 \* 420  
TrMDHc : TCTGAGGTAACGGGTATGCAGGTGAAGAACAGAGCTGGAAAGCTTGAGGGTGCTGAT : 420

\* 440 \* 460 \* 480  
TrMDHc : GTTGTATAATTCCCTGCTGGTGTGCCAGAAAGCCTGGAATGACTCGTGATGATCTTTC : 480

\* 500 \* 520 \* 540  
TrMDHc : AATAITAACGCTGGCATTGTCAAGTCACTTGCCACTGCTATTCTAAGTACTGCCCAT : 540

\* 560 \* 580 \* 600  
TrMDHc : GCCCTTGTAAACATGATAAGCAACCCTGTGAACCTCCACCGTTCCCATTGCTGCAGAGGTT : 600

\* 620 \* 640 \* 660  
TrMDHc : TTCAAGAAGGCAGGGACATATGACGAGAAGAGATTGTTGGGTTACAACCCTTGATGTA : 660

\* 680 \* 700 \* 720  
TrMDHc : GTCAGGGCAAAACTTCTATGCCGGAAAGCTAAAGTTCCAGTTGCCGAGGTCAATGTA : 720

\* 740 \* 760 \* 780  
TrMDHc : CCTGTTATAGGAGGCCATGCAGGAGTTACTATTCTCCATTATTTNTCAGGCAACACCT : 780

\* 800 \* 820 \* 840  
TrMDHc : CAAGCCAATCTGGGTGATGATAACCCTTAAGGNTTAACGGNANGGACACAAGATGGAGGA : 840

\* 860 \* 880 \* 900  
TrMDHc : ACAGAAGTTGNGACCGCCAAGGCTGGAAAGGGTTCTGCAACTTGTCAATGGCTATGCT : 900

\* 920 \* 940 \* 960  
TrMDHc : GGAGCCATATTGCTGATGCTNGCCTCAAAGGNCTGAATGGAGTTCCAGATGTTATTGAG : 960

\* 980 \* 1000 \* 1020  
TrMDHc : TGCTCATATGTGCAATCCAATATCATCTCTGACCTTCCTTCTTGCTTCCAAGGTGAGG : 1020

\* 1040 \* 1060 \* 1080  
TrMDHc : ATTGGGAAGAATGGTGTGAAAGAAATTCTGGGCTTAGGTTCTCACAGATTCGAGCAA : 1080

\* 1100 \* 1120 \* 1140  
TrMDHc : CAAGGCCTTGAAAACCTCAAGGCTGAACCTCAAATCATCTATTGAAAAGGAATCAAATTT : 1140

\* 1160 \* 1180 \* 1200  
TrMDHc : GCCTCCCAGTAATCGAACATGTCATACATTACTGGATTTCCATTAGAACCCAGATCAA : 1200

\* 1220 \* 1240 \* 1260  
TrMDHc : ATTTGCAAATTCAAGAACAAATTGTTGTAATGTTGCCGGTAGGTATAACCCCTAGATTAA : 1260

\* 1280 \* 1300 \* 1320  
TrMDHc : TAAGTAAATCTGCGAGAGCAGTTATTGCTGCAGGGACTGAAATTAAAACCAGTTTAGG : 1320

\* 1340 \* 1360 \* 1380  
TrMDHc : TTGGCCTTCATCGTAATGGCCCTTCATTGTTGCATGNTTCAATATAATGCAATTGAA : 1380

\* 1400  
TrMDHc : GGGTGNTGGNCANCGATAACACANCCCC : 1408

Figure 62 Dededuced amino acid sequence of TrMDHc

\* 20 \* 40 \* 60  
TrMDHc : MRPSMLRSVQSAVRASSHLTRRGYATEPVPERKVAILGAAGGGIGQPLSLLMKLNPLVST : 60

\* 80 \* 100 \* 120  
TrMDHc : LSLYDIAGTPGVAADVSHINSRSEVTGYAGEEEELGKALEGADVVIIPAGVPRKPGMTRDD : 120

\* 140 \* 160 \* 180  
TrMDHc : LFNINAGIVKSLATAISKYCPHALVNMSNPVNSTVPIAAEVFKKAGTYDEKRLFGVTTL : 180

\* 200 \* 220 \* 240  
TrMDHc : DVVRAKTFYAGKAKVPVAEVNVPVIGGHAGVTILPLFXQATPQANLGDDTLKXLXXTQD : 240

\* 260 \* 280 \* 300  
TrMDHc : GGTEVXTAKAGKGSATLSMAYAGAIFADAXLKKLNGVPDVIECSYVQSNIISDLPFFASK : 300

\* 320 \* 340  
TrMDHc : VRIGKNGVEEILGLGSLTDSEQQGLENLKAELKSSIEKGKIKFASQ : 345

Figure 63 Nucleotide sequences of nucleic acid fragments contributing to the consensus contig sequence TrMDHc

	*	20	*	40	*	60	:	
TrMDHc1	:	AAAGNGAATTGGAATNT	CGAC-CTCCATTCCNTACT	TATTTCATTCATGGCTGTCTCT			: 60	
TrMDHc2	:	-GTTNATTGGAATATA	CGCACTCCATTCCATACT	TATTTCATTCATGGCTGTCTCT			: 59	
TrMDHc3	:	-	GNNCATCGA-CAC	TCCCTTACTT	TTTATCGCT		: 42	
TrMDHc4	:	-	-CNACT-CCATTCCNTACTTT	TTTNTNTNCG			: 30	
TrMDHc5	:	-	-GCATCC-TTCCNTACTTT	NTTGNTCGCT			: 27	
TrMDHc6	:	-	-CNTCCATGCCNTACTTT	NTTGNTCGCT			: 27	
TrMDHc7	:	-	-GNTTCCCTTCCCTACTTT	CATTCCATCG			: 27	
TrMDHc8	:	-	-TCCCATTCCNTACTTT	NTTNTNTNCG			: 27	
TrMDHc9	:	-	-TCCATTCCNTACTTT	ATTTNTTCGCT			: 25	
TrMDHc10	:	-	-TCC-TTCCATTACTTT	ATTGATCGCT			: 25	
TrMDHc11	:	-	-	-	-		:	-
TrMDHc12	:	-	-	-	-		:	-
TrMDHc13	:	-	-	-	-		:	-
TrMDHc14	:	-	-	-	-		:	-
TrMDHc15	:	-	-	-	-		:	-
TrMDHc16	:	-	-	-	-		:	-
TrMDHc17	:	-	-	-	-		:	-
	*	80	*	100	*	120	:	
TrMDHc1	:	CTCTCTCTTTTATTCTGAAAAGCTT	TTCAAGCCAACAAACG	AGAGAATAATGAGGCCGTG			: 122	
TrMDHc2	:	CTCTCTCT	T-TATTCTGAAAAGCTTTTCAGCCAAACAAACG	AGAGAATAATGAGGCCGTG			: 119	
TrMDHc3	:	CTCTCTCT	TTTATTCTGAAAAGCTTTTCAGCCAAACAAACG	AGAGAATAATGAGGCCGTG			: 105	
TrMDHc4	:	CTCTCTCTCT	TATTCTGAAAAGCTTTTCAGCCAAACAAACG	AGAGAATAATGAGGCCGTG			: 91	
TrMDHc5	:	CTCTCTC	--TTTATTCTGAAAAGCTTTTCAGCCAAACAAACG	AGAGAATAATGAGGCCGTG			: 88	
TrMDHc6	:	CTCTCTC	--TTTATTCTGAAAAGCTTTTCAGCCAAACAAACG	AGAGAATAATGAGGCCGTG			: 87	
TrMDHc7	:	CTCTCTCT	TTTATTCTGAAAAGCTTTTCAGCCAAACAAACG	AGAGAATAATGAGGCCGTG			: 90	
TrMDHc8	:	CTCTCTCTCT	TTTATTCTGAAAAGCTTTTCAGCCAAACAAACG	AGAGAATAATGAGGCCGTG			: 89	
TrMDHc9	:	CTCTCTCT	TTTATTCTGAAAAGCTTTTCAGCCAAACAAACG	AGAGAATAATGAGGCCGTG			: 87	
TrMDHc10	:	CTCTCTC	--TTTATTCTGAAAAGCTTTTCAGCCAAACAAACG	AGAGAATAATGAGGCCGTG			: 86	
TrMDHc11	:	-	-GNNCTCG-AAGCTTTT	AGCCAAACAAACG	AGAGAATAATGAGGCCGTG		: 48	
TrMDHc12	:	-	-TTCTCGAAAAGCTTTT	AGCCAAACAAACG	AGAGAAATATGAGGCCGTG		: 46	
TrMDHc13	:	-	-TTCTCG-AAGCTTTTCAGCCAAACAAACG	AGAGAAATATGAGGCCGTG			: 48	
TrMDHc14	:	-	-	-	-		:	-
TrMDHc15	:	-	-	-	-		:	-
TrMDHc16	:	-	-	-	-		:	-
TrMDHc17	:	-	-	-	-		:	-
	*	140	*	160	*	180	:	
TrMDHc1	:	ATGCTCAGATCCGTCCAATCAGCCGT	ATCCCGCGCCTCTCTCACCTAAACCCGCCGTGGCTAT				: 185	
TrMDHc2	:	ATGCTCAGATCCGTCCAATCAGCCGT	ATCCCGCGCCTCTCTCACCTAAACCCGCCGTGGCTAT				: 182	
TrMDHc3	:	ATGCTCAGATCCGTCCAATCAGCCGT	ATCCCGCGCCTCTCTCACCTAAACCCGCCGTGGCTAT				: 168	
TrMDHc4	:	ATGCTCAGATC	GTCCAATCAGCCGT	ATCCCGCGCCTCTCTCACCTAAACCCGCCGTGGCTAT			: 154	
TrMDHc5	:	ATG	TCAGATCCGTCCAATCAGCCGT	ATCCCGCGCCTCTCTCACCTAAACCCGCCGTGGCTAT			: 151	
TrMDHc6	:	ATG	TCAGATCCGTCCAATCAGCCGT	ATCCCGCGCCTCTCTCACCTAAACCCGCCGTGGCTAT			: 150	
TrMDHc7	:	ATG	TCAGATCCGTCCAATCAGCCGT	ATCCCGCGCCTCTCTCACCTAAACCCGCCGTGGCTAT			: 153	
TrMDHc8	:	ATG	TCAGATCCGTCCAATCAGCCGT	ATCCCGCGCCTCTCTCACCTAAACCCGCCGTGGCTAT			: 152	
TrMDHc9	:	ATG	TCAGATCCGTCCAATCAGCCGT	ATCCCGCGCCTCTCTCACCTAAACCCGCCGTGGCTAT			: 150	
TrMDHc10	:	ATG	TCAGATCCGTCCAATCAGCCGT	ATCCCGCGCCTCTCTCACCTAAACCCGCCGTGGCTAT			: 149	
TrMDHc11	:	ATG	TCAGATCCGTCCAATCAGCCGT	ATCCCGCGCCTCTCTCACCTAAACCCGCCGTGGCTAT			: 111	
TrMDHc12	:	ATG	TCAGATC	GTCCAATCAGCCGT	ATCCCGCGCCTCTCTCACCTAAACCCGCCGTGGCTAT		: 108	
TrMDHc13	:	ATG	TCAGATC	GTCCAATCAGCCGT	ATCCCGCGCCTCTCTCACCTAAACCCGCCGTGGCTAT		: 111	
TrMDHc14	:	-	-	-	-		:	-
TrMDHc15	:	-	-	-	-		:	-
TrMDHc16	:	-	-	-	-		:	-
TrMDHc17	:	-	-	-	-		:	-

	*	200	*	220	*	240	*	
TrMDHc1	:	GCTACCGAACCAAGTTCCAGAACGCAAGGTGGCCATTCTCGG		GCTGCCGGGGATCGGACAG			:	248
TrMDHc2	:	GCTACCGAACCAAGTTCCAGAACGCAAGGTGGCCATTCTCGG		GCTGCCGGGGATCGGACAG			:	245
TrMDHc3	:	GCTACCGAACCAAGTTCCAGAACGCAAGGTGGCCATTCTCGG		GCTGCCGGGGATCGGACAG			:	231
TrMDHc4	:	GCTACCGAACCAAGTTCCAGAACGCAAGGTGGCCATTCTCGG		GCTGCCGGGGATCGGACAG			:	217
TrMDHc5	:	GCTACCGAACCAAGTTCCAGAACGCAAGGTGGCCATTCTCGG		GCTGCCGGGGATCGGACAG			:	214
TrMDHc6	:	GCTACCGAACCAAGTTCCAGAACGCAAGGTGGCCATTCTCGG		GCTGCCGGGGATCGGACAG			:	213
TrMDHc7	:	GCTACCGAACCAAGTTCCAGAACGCAAGGTGGCCATTCTCGG		GCTGCCGGGGATCGGACAG			:	216
TrMDHc8	:	GCTACCGAACCAAGTTCCAGAACGCAAGGTGGCCATTCTCGG		GCTGCCGGGGATCGGACAG			:	215
TrMDHc9	:	GCTACCGAACCAAGTTCCAGAACGCAAGGTGGCCATTCTCGG		GCTGCCGGGGATCGGACAG			:	213
TrMDHc10	:	GCTACCGAACCAAGTTCCAGAACGCAAGGTGGCCATTCTCGG		GCTGCCGGGGATCGGACAG			:	212
TrMDHc11	:	GCTACCGAACCAAGTTCCAGAACGCAAGGTGGCCATTCTCGG		GCTGCCGGGGATCGGACAG			:	174
TrMDHc12	:	GCTACCGAACCAAGTTCCAGAACGCAAGGTGGCCATTCTCGG		GCTGCCGGGGATCGGACAG			:	171
TrMDHc13	:	GCTACCGAACCAAGTTCCAGAACGCAAGGTGGCCATTCTCGG		GCTGCCGGGGATCGGACAG			:	174
TrMDHc14	:	-----		-----			:	-
TrMDHc15	:	-----		-----			:	-
TrMDHc16	:	-----		-----			:	-
TrMDHc17	:	-----		-----			:	-
	*	260	*	280	*	300	*	
TrMDHc1	:	CCTCTCTCTTCTCATGAAGCTCAACCCTCTCGTTCAACCCTATCTCTTATGATATTGCT					:	311
TrMDHc2	:	CCTCTCTCTTCTCATGAAGCTCAACCCTCTCGTTCAACCCTATCTCTTATGATATTGCT					:	308
TrMDHc3	:	CCTCTCTCTTCTCATGAAGCTCAACCCTCTCGTTCAACCCTATCTCTTATGATATTGCT					:	294
TrMDHc4	:	CCTCTCTCTTCTCATGAAGCTCAACCCTCTCGTTCAACCCTATCTCTTATGATATTGCT					:	280
TrMDHc5	:	CCTCTCTCTTCTCATGAAGCTCAACCCTCTCGTTCAACCCTATCTCTTATGATATTGCT					:	277
TrMDHc6	:	CCTCTCTCTTCTCATGAAGCTCAACCCTCTCGTTCAACCCTATCTCTTATGATATTGCT					:	276
TrMDHc7	:	CCTCTCTCTTCTCATGAAGCTCAACCCTCTCGTTCAACCCTATCTCTTATGATATTGCT					:	279
TrMDHc8	:	CCTCTCTCTTCTCATGAAGCTCAACCCTCTCGTTCAACCCTATCTCTTATGATATTGCT					:	278
TrMDHc9	:	CCTCTCTCTTCTCATGAAGCTCAACCCTCTCGTTCAACCCTATCTCTTATGATATTGCT					:	276
TrMDHc10	:	CCTCTCTCTTCTCATGAAGCTCAACCCTCTCGTTCAACCCTATCTCTTATGATATTGCT					:	275
TrMDHc11	:	CCTCTCTCTTCTCATGAAGCTCAACCCTCTCGTTCAACCCTATCTCTTATGATATTGCT					:	237
TrMDHc12	:	CCTCTCTCTTCTCATGAAGCTCAACCCTCTCGTTCAACCCTATCTCTTATGATATTGCT					:	234
TrMDHc13	:	CCTCTCTCTTCTCATGAAGCTCAACCCTCTCGTTCAACCCTATCTCTTATGATATTGCT					:	237
TrMDHc14	:	-----		-----			:	-
TrMDHc15	:	-----		-----			:	-
TrMDHc16	:	-----		-----			:	-
TrMDHc17	:	-----		-----			:	-
	*	320	*	340	*	360	*	3
TrMDHc1	:	GGAACCCCTGGTTCGCCGCTGATGTCAGCCACATCAACTCCAGATCTGAGGTAACGGGTAT					:	374
TrMDHc2	:	GGAACCCCTGGTTCGCCGCTGATGTCAGCCACATCAACTCCAGATCTGAGGTAACGGGTAT					:	371
TrMDHc3	:	GGAACCCCTGGTTCGCCGCTGATGTCAGCCACATCAACTCCAGATCTGAGGTAACGGGTAT					:	357
TrMDHc4	:	GGAACCCCTGGTTCGCCGCTGATGTCAGCCACATCAACTCCAGATCTGAGGTAACGGGTAT					:	343
TrMDHc5	:	GGAACCCCTGGTTCGCCGCTGATGTCAGCCACATCAACTCCAGATCTGAGGTAACGGGTAT					:	340
TrMDHc6	:	GGAACCCCTGGTTCGCCGCTGATGTCAGCCACATCAACTCCAGATCTGAGGTAACGGGTAT					:	339
TrMDHc7	:	GGAACCCCTGGTTCGCCGCTGATGTCAGCCACATCAACTCCAGATCTGAGGTAACGGGTAT					:	342
TrMDHc8	:	GGAACCCCTGGTTCGCCGCTGATGTCAGCCACATCAACTCCAGATCTGAGGTAACGGGTAT					:	341
TrMDHc9	:	GGAACCCCTGGTTCGCCGCTGATGTCAGCCACATCAACTCCAGATCTGAGGTAACGGGTAT					:	339
TrMDHc10	:	GGAACCCCTGGTTCGCCGCTGATGTCAGCCACATCAACTCCAGATCTGAGGTAACGGGTAT					:	338
TrMDHc11	:	GGAACCCCTGGTTCGCCGCTGATGTCAGCCACATCAACTCCAGATCTGAGGTAACGGGTAT					:	300
TrMDHc12	:	GGAACCCCTGGTTCGCCGCTGATGTCAGCCACATCAACTCCAGATCTGAGGTAACGGGTAT					:	297
TrMDHc13	:	GGAACCCCTGGTTCGCCGCTGATGTCAGCCACATCAACTCCAGATCTGAGGTAACGGGTAT					:	300
TrMDHc14	:	-----ENGTGTCGCCGCTGNNGTCAGCCACATCAACTCCANACTGA-GTAACGGGTAT					:	54
TrMDHc15	:	-----GNTGATGT-NGCC-CAT-AACTCC-GATCTGAGGTAACGGGTAT					:	41
TrMDHc16	:	-----		-----			:	-
TrMDHc17	:	-----		-----			:	-

	80	*	400	*	420	*	440	:	
TrMDHc1	: GCAGGTGAAGAAGAGCTTGGAAAAGCTTGGAGGGTGCATGTTGTATAATTCCCTGCTGGT							: 437	
TrMDHc2	: GCAGGTGAAGAAGAGCTTGGAAAAGCTTGGAGGGTGCATGTTGTATAATTCCCTGCTGGT							: 434	
TrMDHc3	: GCAGGTGAAGAAGAGCTTGGAAAAGCTTGGAGGGTGCATGTTGTATAATTCCCTGCTGGT							: 420	
TrMDHc4	: GCAGGTGAAGAAGAGCTTGGAAAAGCTTGGAGGGTGCATGTTGTATAATTCCCTGCTGGT							: 406	
TrMDHc5	: GCAGGTGAAGAAGAGCTTGGAAAAGCTTGGAGGGTGCATGTTGTATAATTCCCTGCTGGT							: 403	
TrMDHc6	: GCAGGTGAAGAAGAGCTTGGAAAAGCTTGGAGGGTGCATGTTGTATAATTCCCTGCTGGT							: 402	
TrMDHc7	: GCAGGTGAAGAAGAGCTTGGAAAAGCTTGGAGGGTGCATGTTGTATAATTCCCTGCTGGT							: 405	
TrMDHc8	: GCAGGTGAAGAAGAGCTTGGAAAAGCTTGGAGGGTGCATGTTGTATAATTCCCTGCTGGT							: 404	
TrMDHc9	: GCAGGTGAAGAAGAGCTTGGAAAAGCTTGGAGGGTGCATGTTGTATAATTCCCTGCTGGT							: 402	
TrMDHc10	: GCAGGTGAAGAAGAGCTTGGAAAAGCTTGGAGGGTGCATGTTGTATAATTCCCTGCTGGT							: 401	
TrMDHc11	: GCAGGTGAAGAAGAGCTTGGAAAAGCTTGGAGGGTGCATGTTGTATAATTCCCTGCTGGT							: 363	
TrMDHc12	: GCAGGTGAAGAAGAGCTTGGAAAAGCTTGGAGGGTGCATGTTGTATAATTCCCTGCTGGT							: 360	
TrMDHc13	: GCAGGTGAAGAAGAGCTTGGAAAAGCTTGGAGGGTGCATGTTGTATAATTCCCTGCTGGT							: 363	
TrMDHc14	: GCAGGTGAAGAAGAGCTTGGAAAAGCTTGGAGGGTGCATGTTGTATAATTCCCTGCTGGT							: 117	
TrMDHc15	: GCAGGTGAAGAAGAGCTTGGAAAAGCTTGGAGGGTGCATGTTGTATAATTCCCTGCTGGT							: 104	
TrMDHc16	: -----							:	-
TrMDHc17	: -----							:	-
	*	460	*	480	*	500	:		
TrMDHc1	: GTGCCCGAGAAAGCCTGGAATGACTCGTGTATCTTTCAATATTAAACGCTGGCATTGTCAAG							: 500	
TrMDHc2	: GTGCCCGAGAAAGCCTGGAATGACTCGTGTATCTTTCAATATTAAACGCTGGCATTGTCAAG							: 497	
TrMDHc3	: GTGCCCGAGAAAGCCTGGAATGACTCGTGTATCTTTCAATATTAAACGCTGGCATTGTCAAG							: 483	
TrMDHc4	: GTGCCCGAGAAAGCCTGGAATGACTCGTGTATCTTTCAATATTAAACGCTGGCATTGTCAAG							: 469	
TrMDHc5	: GTGCCCGAGAAAGCCTGGAATGACTCGTGTATCTTTCAATATTAAACGCTGGCATTGTCAAG							: 466	
TrMDHc6	: GTGCCCGAGAAAGCCTGGAATGACTCGTGTATCTTTCAATATTAAACGCTGGCATTGTCAAG							: 465	
TrMDHc7	: GTGCCCGAGAAAGCCTGGAATGACTCGTGTATCTTTCAATATTAAACGCTGGCATTGTCAAG							: 468	
TrMDHc8	: GTGCCCGAGAAAGCCTGGAATGACTCGTGTATCTTTCAATATTAAACGCTGGCATTGTCAAG							: 467	
TrMDHc9	: GTGCCCGAGAAAGCCTGGAATGACTCGTGTATCTTTCAATATTAAACGCTGGCATTGTCAAG							: 465	
TrMDHc10	: GTGCCCGAGAAAGCCTGGAATGACTCGTGTATCTTTCAATATTAAACGCTGGCATTGTCAAG							: 464	
TrMDHc11	: GTGCCCGAGAAAGCCTGGAATGACTCGTGTATCTTTCAATATTAAACGCTGGCATTGTCAAG							: 426	
TrMDHc12	: GTGCCCGAGAAAGCCTGGAATGACTCGTGTATCTTTCAATATTAAACGCTGGCATTGTCAAG							: 423	
TrMDHc13	: GTGCCCGAGAAAGCCTGGAATGACTCGTGTATCTTTCAATATTAAACGCTGGCATTGTCAAG							: 426	
TrMDHc14	: GTGCCCGAGAAAGCCTGGAATGACTCGTGTATCTTTCAATATTAAACGCTGGCATTGTCAAG							: 180	
TrMDHc15	: GTGCCCGAGAAAGCCTGGAATGACTCGTGTATCTTTCAATATTAAACGCTGGCATTGTCAAG							: 167	
TrMDHc16	: -----							:	-
TrMDHc17	: -----							:	-
	*	520	*	540	*	560	:		
TrMDHc1	: TCACCTGCCACTGCTATTCTAACGTAAGTACTGCCCATG-----							: 537	
TrMDHc2	: TCACCTGCCACTGCTATTCTAACGTAAGTACTGCCCATGCCCTGTTAACATGATAAGCAACCT							: 560	
TrMDHc3	: TCACCTGCCACTGCTATTCTAACGTAAGTACTGCCCATGCCCTGTTAACATGATAAGCAACCT							: 546	
TrMDHc4	: TCACCTGCCACTGCTATTCTAACGTAAGTACTGCCCATGCCCTGTTAACATGATAAGCAACCT							: 532	
TrMDHc5	: TCACCTGCCACTGCTATTCTAACGTAAGTACTGCCCATGCCCTGTTAACATGATAAGCAACCT							: 529	
TrMDHc6	: TCACCTGCCACTGCTATTCTAACGTAAGTACTGCCCATGCCCTGTTAACATGATAAGCAACCT							: 528	
TrMDHc7	: TCACCTGCCACTGCTATTCTAACGTAAGTACTGCCCATGCCCTGTTAACATGATAAGCAACCT							: 531	
TrMDHc8	: TCACCTGCCACTGCTATTCTAACGTAAGTACTGCCCATGCCCTGTTAACATGATAAGCAACCT							: 530	
TrMDHc9	: TCACCTGCCACTGCTATTCTAACGTAAGTACTGCCCATGCCCTGTTAACATGATAAGCAACCT							: 528	
TrMDHc10	: TCACCTGCCACTGCTATTCTAACGTAAGTACTGCCCATGCCCTGTTAACATGATAAGCAACCT							: 527	
TrMDHc11	: TCACCTGCCACTGCTATTCTAACGTAAGTACTGCCCATGCCCTGTTAACATGATAAGCAACCT							: 489	
TrMDHc12	: TCACCTGCCACTGCTATTCTAACGTAAGTACTGCCCATGCCCTGTTAACATGATAAGCAACCT							: 486	
TrMDHc13	: TCACCTGCCACTGCTATTCTAACGTAAGTACTGCCCATGCCCTGTTAACATGATAAGCAACCT							: 489	
TrMDHc14	: TCACCTGCCACTGCTATTCTAACGTAAGTACTGCCCATGCCCTGTTAACATGATAAGCAACCT							: 243	
TrMDHc15	: TCACCTGCCACTGCTATTCTAACGTAAGTACTGCCCATGCCCTGTTAACATGATAAGCAACCT							: 230	
TrMDHc16	: -----							: 3	
TrMDHc17	: -----							:	-

	* 580	* 600	* 620	*	
TrMDHc1	:				
TrMDHc2	: GTGAACTCCACC GTTCCCATTGCTGCAGAGGT TTCAAGAAGGCAGGG-----				608
TrMDHc3	: GTGAACTCCACC GTTCCCATTGCTGCAGG-----				575
TrMDHc4	: GTGAACTCCACC GTTCCCATTGCTGCAGAGG-----				563
TrMDHc5	: GTGAACTCCACC GTTCCCATTGCTGCAGAGGT TTCAAGAAGGCAGGGACATAT-----				583
TrMDHc6	: GTGAACTCCACC GTTCCCATTGCTGCAGAGGT TTCAAGAAGGCAGGGACATATGACGAGAAG-----				591
TrMDHc7	: GTGAACTCCACC GTTCCCATTGCTGCAGAGGT TTCAAGAAGGCAGGGACATATGACGAGAAG-----				594
TrMDHc8	: GTGAACTCCACC GTTCCCATTGCTGC-----				556
TrMDHc9	: GTGAACTCCACC GTTCCCATTGCTGCAGAGGT TTCAAGAAGGCAGGGACATATGACGAGAAG-----				591
TrMDHc10	: GTGAACTCCACC GTTCCCATTGCTGAGAGGT TTCAAGAAGGCAGGGACATATGACGAGAAG-----				590
TrMDHc11	: GTGAACTCCACC GTTCCCATTGCTGCAGAGGT TTCAAGAAGGCAGGGACATATGACGAGAAG-----				552
TrMDHc12	: GTGAACTCCACC GTTCCCATTGCTGCAGAGGT TTCAAGAAGGCAGGGACATATGACGAGAAG-----				549
TrMDHc13	: GTGAACTCCACC GTTCCCATTGCTGAGAGGT TTCAAGAAGGCAGGGACATATGACGAGAAG-----				552
TrMDHc14	: GTGAACTCCACC GTTCCCATTGCTGCAGAGGT TTCAAGAAGGCAGGGACATATGACGAGAAG-----				306
TrMDHc15	: GTGAACTCCACC GTTCCCATTGCTGCAGAGGT TTCAAGAAGGCAGGGACATATGACGAGAAG-----				293
TrMDHc16	:				-
TrMDHc17	:				-
	640	* 660	* 680	*	
TrMDHc1	:				
TrMDHc2	:				-
TrMDHc3	:				-
TrMDHc4	:				-
TrMDHc5	:				-
TrMDHc6	: AGATTGT-----				598
TrMDHc7	: AGATTGTTGGGGTTACAACCCTTGATGTAGTCAGGGC GAAA ACTTTCTATGCCGGGAAAGCT-----				657
TrMDHc8	:				-
TrMDHc9	: AGATTGTTGGGGTTACAACCCTTGATGTAGTCAGGGC GAAA ACTTTCTATGCCGGGAAAGCT-----				654
TrMDHc10	: AGATTGTTGGGGTTACAACCCTTGATGTAGTCAGGGC GAAA ACTTTCTATGCCGGGAAAGCT-----				652
TrMDHc11	: AGATTGTTGGGGTTACAACCCTTG-----				577
TrMDHc12	: AGATTGTTGGGGTTACAACCCTTGATGTAGTCAGGGCAAAACT-----				594
TrMDHc13	: AGATTGTTGGGGTTACAACCCTTGATGTAGTCAGGGCAAAACTTTCTATGCCGGGAAAGCT-----				615
TrMDHc14	: AGATTGTTGGGGTTACAACCCTTGATGTAGTCAGGGCAAAACTTTCTATGCCGGGAAAGCT-----				369
TrMDHc15	: AGATTGTTGGGGTTACAACCCTTGATGTAGTCAGGGCAAAACTTTCTATGCCGGGAAAGCT-----				356
TrMDHc16	:				-
TrMDHc17	:				-
	700	* 720	* 740	*	
TrMDHc1	:				
TrMDHc2	:				-
TrMDHc3	:				-
TrMDHc4	:				-
TrMDHc5	:				-
TrMDHc6	:				-
TrMDHc7	: AAAGTTCCAGTTGCCGAGGTCAATGTACCTGTT TGGAGGCCATGCAGGAGTTACTATTNT-----				720
TrMDHc8	:				-
TrMDHc9	: AAAGTTCCAGTTGCCGAGGTCAATGTAC-----				682
TrMDHc10	: AAAGTTCCAGTTGCCGAGGTCAATGTACCTGTT TGGAGGCC-TGG-NGAG-TNCTATT-NT-----				711
TrMDHc11	:				-
TrMDHc12	:				-
TrMDHc13	: AAAGTTCCAGTTGCCGAGGTCAATGTACCTGTTAGGAGGCCATGCAGGAGTTACTATTCT-----				678
TrMDHc14	: AAAGTTCCAGTTGCCGAGGTCAATGTACCTGTTAGGAGGCCATGCAGGAGTTACTATTCT-----				432
TrMDHc15	: AAAGTTCCAGTTGCCGAGGTCAATGTACCTGTTAGGAGGCCATGCAGGAGTTACTATTCT-----				419
TrMDHc16	:				-
TrMDHc17	:				-

	760	*	780	*	800	*	82
TrMDHc1	:	-	-	-	-	-	-
TrMDHc2	:	-	-	-	-	-	-
TrMDHc3	:	-	-	-	-	-	-
TrMDHc4	:	-	-	-	-	-	-
TrMDHc5	:	-	-	-	-	-	-
TrMDHc6	:	-	-	-	-	-	-
TrMDHc7	:	CCATTATTTNT	AAGG	AACACCTNAAGCCAATNTGGGTGATGA	ACCCCTTNAAGGNTTAA	ACG	782
TrMDHc8	:	-	-	-	-	-	-
TrMDHc9	:	-	-	-	-	-	-
TrMDHc10	:	CCGTTTTTTT	AAGG	GANNCCT-NANCCANT-TNGGNATNAAA-CCTTAAGG	TTT	ACG	769
TrMDHc11	:	-	-	-	-	-	-
TrMDHc12	:	-	-	-	-	-	-
TrMDHc13	:	CCATTATTTNT	NAGGCAACACCTNAAGCCAATNTGGGTGANGATN	CCCTTAAGGNTTAA	ACG	741	
TrMDHc14	:	CCATTATTTCT	CAGGCAACACCTCAAGCCAATCTGG	TGATGATACCA	TTAAGGCT	TAACG	495
TrMDHc15	:	CCATTATTTCT	CAGGCAACACCTCAAGCCAATCTGG	TGATGATACCA	TTAAGGCT	TAACG	482
TrMDHc16	:	-	-	-	-	-	-
TrMDHc17	:	-	-	-	-	-	-

	0	*	840	*	860	*	880	
TrMDHc1	:							:
TrMDHc2	:							:
TrMDHc3	:							:
TrMDHc4	:							:
TrMDHc5	:							:
TrMDHc6	:							:
TrMDHc7	:	GNANGGCNCAAGATGGGGAAACNGAA		TTGNGACC GCCAAGGGT				827
TrMDHc8	:							:
TrMDHc9	:							:
TrMDHc10	:	GS	NNGGC NCAAAANG	GGGAACACAAA	NTNGAC			801
TrMDHc11	:							:
TrMDHc12	:							:
TrMDHc13	:	GNANGGAC	CAAN	ANGGAGGAAC	CAAN	ANTT	NNACT	801
TrMDHc14	:	GCAAGG	GACACAAGAT	GGGAGGAAC	CAGAAC	TGTG	TGACCGCCAAGGCT	558
TrMDHc15	:	GCAAGG	GACACAAGAT	GGGAGGAAC	CAGAAC	GTG	TGACCGCCAAGGCT	545
TrMDHc16	:							:
TrMDHc17	:							:

	*	900	*	920	*	940
TrMDHc1	:	-	-	-	-	-
TrMDHc2	:	-	-	-	-	-
TrMDHc3	:	-	-	-	-	-
TrMDHc4	:	-	-	-	-	-
TrMDHc5	:	-	-	-	-	-
TrMDHc6	:	-	-	-	-	-
TrMDHc7	:	-	-	-	-	-
TrMDHc8	:	-	-	-	-	-
TrMDHc9	:	-	-	-	-	-
TrMDHc10	:	-	-	-	-	-
TrMDHc11	:	-	-	-	-	-
TrMDHc12	:	-	-	-	-	-
TrMDHc13	:	TT-[NNAATGGN]-	-	-	-	-
TrMDHc14	:	TTGTCAATGGCT	TATGCTGGAGCCAT	ATTGCTGATGCT	[GCCTCAAAGG]-	CTGAATGGAGTT
TrMDHc15	:	TTGTCAATGGCT-	-	-	-	-
TrMDHc16	:	-	-	CTGNTGCTNGCCT-	NANGGNCTGAATGGAGTT	-
TrMDHc17	:	-	-	-	-	GNGNGTT

	*      960	*      980	*      1000					
TrMDHc1	:	-	-	:				
TrMDHc2	:	-	-	:				
TrMDHc3	:	-	-	:				
TrMDHc4	:	-	-	:				
TrMDHc5	:	-	-	:				
TrMDHc6	:	-	-	:				
TrMDHc7	:	-	-	:				
TrMDHc8	:	-	-	:				
TrMDHc9	:	-	-	:				
TrMDHc10	:	-	-	:				
TrMDHc11	:	-	-	:				
TrMDHc12	:	-	-	:				
TrMDHc13	:	-	-	:				
TrMDHc14	:	<b>CCAGATGTTATTGAGTGCTCATATGTCAATCCAATATCATCTCTGA</b>	<b>CCTT</b>	<b>NCTTTCTTGCT</b>	<b>684</b>			
TrMDHc15	:	-	-	-	-			
TrMDHc16	:	<b>-CNGANGTTATTGAA</b>	<b>GCTCATATGTCAATCCAATATCATCT</b>	<b>N</b>	<b>GACCTTCCTTCTTGCT</b>	<b>96</b>		
TrMDHc17	:	<b>CCAGATGTTATTGAGTGCT</b>	<b>-NTATGTGC</b>	<b>-AT</b>	<b>CNATAT</b>	<b>-NTCTCTGAC</b>	<b>CCTTCCTTCTTGCT</b>	<b>66</b>
	*      1020	*      1040	*      1060	*				
TrMDHc1	:	-	-	-	:			
TrMDHc2	:	-	-	-	:			
TrMDHc3	:	-	-	-	:			
TrMDHc4	:	-	-	-	:			
TrMDHc5	:	-	-	-	:			
TrMDHc6	:	-	-	-	:			
TrMDHc7	:	-	-	-	:			
TrMDHc8	:	-	-	-	:			
TrMDHc9	:	-	-	-	:			
TrMDHc10	:	-	-	-	:			
TrMDHc11	:	-	-	-	:			
TrMDHc12	:	-	-	-	:			
TrMDHc13	:	-	-	-	:			
TrMDHc14	:	<b>TCCAAGGTGAGGATTGGGA</b>	<b>A</b>	<b>NAATGGTGTGGGA</b>	<b>ANAAT</b>	<b>722</b>		
TrMDHc15	:	-	-	-	-	-		
TrMDHc16	:	<b>TCCAAGGNNNNGATTGGGA</b>	<b>AGAATGGTGTGGGA</b>	<b>AGAGATTCTG</b>	-	<b>138</b>		
TrMDHc17	:	<b>TCC</b>	<b>-AGGTGAGGATTGGGA</b>	<b>AGAATGGTGTGGGA</b>	<b>AGAAATTCTGGGCTT</b>	<b>AGGTTCTCTCACAGAT</b>	<b>128</b>	
	1080	*      1100	*      1120	*				
TrMDHc1	:	-	-	-	:			
TrMDHc2	:	-	-	-	:			
TrMDHc3	:	-	-	-	:			
TrMDHc4	:	-	-	-	:			
TrMDHc5	:	-	-	-	:			
TrMDHc6	:	-	-	-	:			
TrMDHc7	:	-	-	-	:			
TrMDHc8	:	-	-	-	:			
TrMDHc9	:	-	-	-	:			
TrMDHc10	:	-	-	-	:			
TrMDHc11	:	-	-	-	:			
TrMDHc12	:	-	-	-	:			
TrMDHc13	:	-	-	-	:			
TrMDHc14	:	-	-	-	:			
TrMDHc15	:	-	-	-	:			
TrMDHc16	:	-	-	-	:			
TrMDHc17	:	<b>TTCGAGCAACAAGGCCTTGA</b>	<b>AAAACCTCAAGGCTGA</b>	<b>ACTCAAATCATCTATTG</b>	<b>AAAAGGGAATC</b>	<b>191</b>		

	1140	*	1160	*	1180	*	1
TrMDHc1	:						
TrMDHc2	:						
TrMDHc3	:						
TrMDHc4	:						
TrMDHc5	:						
TrMDHc6	:						
TrMDHc7	:						
TrMDHc8	:						
TrMDHc9	:						
TrMDHc10	:						
TrMDHc11	:						
TrMDHc12	:						
TrMDHc13	:						
TrMDHc14	:						
TrMDHc15	:						
TrMDHc16	:						
TrMDHc17	:	AAATTGCCTCCAGTAATCGAACATGTCATACTACATTACTGGATTTCCATTAGAACAGAT					254

	200	*	1220	*	1240	*	1260
TrMDHc1	:						
TrMDHc2	:						
TrMDHc3	:						
TrMDHc4	:						
TrMDHc5	:						
TrMDHc6	:						
TrMDHc7	:						
TrMDHc8	:						
TrMDHc9	:						
TrMDHc10	:						
TrMDHc11	:						
TrMDHc12	:						
TrMDHc13	:						
TrMDHc14	:						
TrMDHc15	:						
TrMDHc16	:						
TrMDHc17	:	CAAATTTGCAAATTCAAGAACATTGTTGTAATGTTGCCGGTAGGTACCCCTAGATTAA					317

	*	1280	*	1300	*	1320	
TrMDHc1	:						
TrMDHc2	:						
TrMDHc3	:						
TrMDHc4	:						
TrMDHc5	:						
TrMDHc6	:						
TrMDHc7	:						
TrMDHc8	:						
TrMDHc9	:						
TrMDHc10	:						
TrMDHc11	:						
TrMDHc12	:						
TrMDHc13	:						
TrMDHc14	:						
TrMDHc15	:						
TrMDHc16	:						
TrMDHc17	:	TAAGTAAATCTGCGAGAGCAGTTATTGCTGCAGGGACTGAAATTAAACCAGTTTAGGTTG					380

	*	1340	*	1360	*	1380	
TrMDHc1	:	-	-	-	-	-	:
TrMDHc2	:	-	-	-	-	-	:
TrMDHc3	:	-	-	-	-	-	:
TrMDHc4	:	-	-	-	-	-	:
TrMDHc5	:	-	-	-	-	-	:
TrMDHc6	:	-	-	-	-	-	:
TrMDHc7	:	-	-	-	-	-	:
TrMDHc8	:	-	-	-	-	-	:
TrMDHc9	:	-	-	-	-	-	:
TrMDHc10	:	-	-	-	-	-	:
TrMDHc11	:	-	-	-	-	-	:
TrMDHc12	:	-	-	-	-	-	:
TrMDHc13	:	-	-	-	-	-	:
TrMDHc14	:	-	-	-	-	-	:
TrMDHc15	:	-	-	-	-	-	:
TrMDHc16	:	-	-	-	-	-	:
TrMDHc17	:	GCCTTCCATTGTAATGCCCTTCATTGTTGCATGNTTCATATA@TGCAATTGAAGGGTGN	:	443			

	*	1400				
TrMDHc1	:	-	-			
TrMDHc2	:	-	-			
TrMDHc3	:	-	-			
TrMDHc4	:	-	-			
TrMDHc5	:	-	-			
TrMDHc6	:	-	-			
TrMDHc7	:	-	-			
TrMDHc8	:	-	-			
TrMDHc9	:	-	-			
TrMDHc10	:	-	-			
TrMDHc11	:	-	-			
TrMDHc12	:	-	-			
TrMDHc13	:	-	-			
TrMDHc14	:	-	-			
TrMDHc15	:	-	-			
TrMDHc16	:	-	-			
TrMDHc17	:	TGGNCANCGATAACACANCCCC	:	465		

Figure 64 Consensus contig nucleotide sequence of TrMDHd

\* 20 \* 40 \* 60  
TrMDHd : GGGTAGGCAGATTNAACCCATTTCTCTAAATCTCTCAACTCTCTTCCATT : 60

\* 80 \* 100 \* 120  
TrMDHd : CCCATTACCATTCCCAGAGGTCGAGATGGCAGCATCAGCAGCTACTTTACTA : 120

\* 140 \* 160 \* 180  
TrMDHd : TTGGAAC TGCCAAACAGGGAGGCCACTCCTCAATCAAACCCTTGGTTGAAAGTCA : 180

\* 200 \* 220 \* 240  
TrMDHd : ATTCCCAGGTTAATTAAAGACCTTCTCTGGTCTCAAGGCCATGTCATCTCTAAAGATGCG : 240

\* 260 \* 280 \* 300  
TrMDHd : AGTCTGAATCATCTTCTTGCAACGAAACTAGTGCTGCTCTGCGTGCAACTTTGCAC : 300

\* 320 \* 340 \* 360  
TrMDHd : CCAAAGCTCAAAAGGAAAACCAAAACATCAACCGCAATTGCATCCTCAGGCATCCTACA : 360

\* 380 \* 400 \* 420  
TrMDHd : AAGTGGCGGTCTTGGTGCTGCAGGAGGAATTGGTCAGCCACTGGCACTCTCATTAAGA : 420

\* 440 \* 460 \* 480  
TrMDHd : TGTCGCCTTGGTTCCGACCTGCATCTTATGATATCGCGAATGTTAAGGGAGTTGCTG : 480

\* 500 \* 520 \* 540  
TrMDHd : CTGATATCAGTCATTGCAACACTCCTCAAAGGTTGGATTCACAGGTGCTCTGAGT : 540

\* 560 \* 580 \*  
TrMDHd : TGGCAAATTGTTGAAAGGTGTGGATGTAGTTGTTACCTGCTGGTGTCCCAGAAA : 598

Figure 65 Deducing amino acid sequence of TrMDhd

\* 20 \* 40 \* 60  
TrMDhd : MAASAAATFTIGTAQTGRPLPQSNPFGLKVNQVNFKTFSGLKAMSSLRCESESSFFGNE : 60

\* 80 \* 100 \* 120  
TrMDhd : TSAALRATFAPKAQKENQNINRNLHPQASYKVAVLGAAGGIGQPLALLIKMSPLVSDLHL : 120

\* 140 \* 160  
TrMDhd : YDIANVKGVAADISHCNTPSKVLDFTGASELANCLKGVVVIPAGVPR : 169

Figure 66 Nucleotide sequences of nucleic acid fragments contributing to the consensus contig sequence TrMDHd

	*	20	*	40	*	60	
TrMDHd1	:	CNCTAGGCGGAGATTNAACCCATTTCCTCTAAATCTCTCTAAACTCTCTTTCCATT					: 60
TrMDHd2	:	-GTTAGGCGGAGATTNAACCCATTTCCTCTAAATCTCTCTC-ACTTCTCTTTCCATT					: 58
TrMDHd3	:	-----GGAGATTNAACCCATTTCCTCTAAATCTCTC-CGACTCTCTCGTTCCATT					: 52
	*	80	*	100	*	120	
TrMDHd1	:	CCCATTACCATTCATTCCCAGAGGGTCGAGATGGCAGCAGCATCAGCAGCAGCTACTTTACTA					: 120
TrMDHd2	:	CCCATTACCATTCATTCCCAGAGGGTCGAGATGGCAGCAGCATCAGCAGCAGCTACTTTACTA					: 118
TrMDHd3	:	CCCATTACCATTCATTCCCAGAGGTGAGATGGCAGCAGCATCAGCAGCAGCTACTTTACTA					: 112
	*	140	*	160	*	180	
TrMDHd1	:	TTGGAACTGCCAACACAGGGAGGCCACTTCCTCAATCAAACCCTTTGTTGAAAGTCA					: 180
TrMDHd2	:	TTGGAACTGCCAACACAGGGAGGCCACTTCCTCAATCAAACCCTTTGTTGAAAGTCA					: 178
TrMDHd3	:	TTGGAACTGCCAACACAGGGAGGCCACTTCCTCAATCAAACCCTTTGTTGAAAGTCA					: 172
	*	200	*	220	*	240	
TrMDHd1	:	ATTCCCAGGTTAATTAAAGACCTTCTGGTCTCAAGGCCATGTCACTCTAAAGATGCG					: 240
TrMDHd2	:	ATTCCCAGGTTAATTAAAGACCTTCTGGTCTCAAGGCCATGTCACTCTAAAGATGCG					: 238
TrMDHd3	:	ATTCCCAGGTTAATTAAAGACCTTCTGGTCTCAAGGCCATGTCACTCTAAAGATGCG					: 232
	*	260	*	280	*	300	
TrMDHd1	:	AGTCTGAATCATCTTCTTGCAACGAAACTAGTGCTGCTCTGCGTCAACTTTGCAC					: 300
TrMDHd2	:	AGTCTGAATCATCTTCTTGCAACGAAACTAGTGCTGCTCTGCGTCAACTTTGCAC					: 298
TrMDHd3	:	AGTCTGAATCATCTTCTTGCAACGAAACTAGTGCTGCTCTGCGTCAACTTTGCAC					: 292
	*	320	*	340	*	360	
TrMDHd1	:	CCAAAGCTAAAAGGAAAACCACATCAACCGCAATTGCACTCCTAGGCATCCTACA					: 360
TrMDHd2	:	CCAAAGCTAAAAGGAAAACCACATCAACCGCAATTGCACTCCTAGGCATCCTACA					: 358
TrMDHd3	:	CCAAAGCTAAAAGGAAAACCACATCAACCGCAATTGCACTCCTAGGCATCCTACA					: 352
	*	380	*	400	*	420	
TrMDHd1	:	AAGTGGCGTTCTGGTCTGCAGGAGGAATTGGTCAGCCACTGGCAGTTCTCATTAAGA					: 420
TrMDHd2	:	AAGTGGCGTTCTGGTCTGCAGGAGGAATTGGTCAGCCACTGGCAGTTCTCATTAAGA					: 418
TrMDHd3	:	AAGTGGCGTTCTGGTCTGCAGGAGGAATTGGTCAGCCACTGGCAGTTCTCATTAAGA					: 412
	*	440	*	460	*	480	
TrMDHd1	:	TGTCGCCTTGGTTCCGACCTGCATCTTATGATATCGCGAATGTTAGGGAGTTGCTG					: 480
TrMDHd2	:	TGTCGCCTTGGTTCCGACCTGCATCTTATGATATCGCGAATGTTAGGGAGTTGCTG					: 478
TrMDHd3	:	TGTCGCCTTGGTTCCGACCTGCATCTTATGATATCGCGAATGTTAGGGAGTTGCTG					: 472
	*	500	*	520	*	540	
TrMDHd1	:	CTGATATCAGTCATTGCAACACTCCTCAAAGGTTTGAGTTCACAGGTGCTTCTGAGT					: 540
TrMDHd2	:	CTGATATCAGTCATTGCAACACTCCTCAAAGGTTTGAGTTCACAGGTGCTTCTGAGT					: 538
TrMDHd3	:	CTGATATCAGTCATTGCAACACTCCTCAAAGGTTTGAGTTCACAGGTGCTTCTGAGT					: 532
	*	560	*	580	*		
TrMDHd1	:	TGGCAAATTGTTTG-----					: 554
TrMDHd2	:	TGGCAAATTGTTTGAAAGGTGTGGATGTAGTTGTTACACCTGCTGGTGTCCCAG-----					: 593
TrMDHd3	:	TGGCAAATTGTTGAAAGGTGTGGATGTGTTGTTACACCTGCTGGTGTCCCAGAAA-----					: 590

Figure 67 Consensus contig nucleotide sequence of TrMDHe

\* 20 \* 40 \* 60  
TrMDHe : TTNTNTTATTATGTTTTNCCTCCTACATATAACTCTNACTTNGCATACACTGTG : 60

\* 80 \* 100 \* 120  
TrMDHe : TCTCTCAATTATTATTAGTCCTTAGAAATGGAAGCACATGCAGCTGGAGCCAATCAGAGG : 120

\* 140 \* 160 \* 180  
TrMDHe : ATTGCAAGAACCTCTGCTCATCTCAACCTCCAAATTCCAGGAAGGAGGTGATGTTGCA : 180

\* 200 \* 220 \* 240  
TrMDHe : ATTAGCAAAGCTAAGCAGAGCAAAAGGTGGGGCGCCGGGATTCAAAGTAGCAATCTTG : 240

\* 260 \* 280 \* 300  
TrMDHe : GGGGCTGCTGGTGGATTGGTCAATCCCTTCTTGCTGTTGAAGATCAATCCATTGGTT : 300

\* 320 \* 340 \* 360  
TrMDHe : TCAGTTCTTCATCTTATGATGTTGTCAACACTCCTGGTGTCACTGCTGATGTTAGTCAC : 360

\* 380 \* 400 \* 420  
TrMDHe : ATTGACACCGGTGCTGTTGCTGGCTTCTAGGGCAGGCACAATTGAGAATGCACTT : 420

\* 440 \* 460 \* 480  
TrMDHe : ACAGGCATGGACTTGGTCGTTACCTGCTGGTGTGCCGAGGAAACCTGGAATGACAAGG : 480

\* 500 \* 520 \* 540  
TrMDHe : GATGACTTATTAAGATAAAATGCTGGAATTGTGAGGACTCTAGCGAAGGAATTGCCAAG : 540

\* 560 \* 580 \* 600  
TrMDHe : AGCTGTCCTAATGCAATTGCAACTTGTGATTAGCAATCCAGTGAATTCCACTGTGCCAATT : 600

\* 620 \* 640 \* 660  
TrMDHe : GCTGCTGAGGTTTCAAGAAAGCCGGTACATATGATCCAAAGCGACTTTAGGGTTACA : 660

\* 680 \* 700 \* 720  
TrMDHe : ACCCTCGATGTTGTGAGGGCAAATACCTTGTGGCAGAAGTACTTGGTGTGATCCAAGA : 720

\* 740 \* 760 \* 780  
TrMDHe : GAGGTTGATGTTCCAGTGGTAGGAGGGCACGCAGGAGTCACAATATTACCTCTTGTCA : 780

\* 800 \* 820 \* 840  
TrMDHe : CAGGTTAACGCCTCCCAGTAGCTTACCGCAGAAGAACCGAATACCTGACAAANCAGCATT : 840

\* 860 \* 880 \* 900  
TrMDHe : CAAAANGCGGAACACAAGTTGTTGAGGCAAAGGCTGGGCTGGTTCGGCAACACTANTN : 900

\* 920 \* 940 \* 960  
TrMDHe : ATGGCCTATGCAGCTGCCAACGTTGCTAACGCATGCCTCCGTGGCTGAAAGGAGAAGCC : 960

\* 980 \* 1000 \* 1020  
rMDHe : GGGATAGTGGAGTGTGCTTTGTTGATTCTCAGGTTACGGAACCTCCTTCAGCC : 1020

\* 1040 \* 1060 \* 1080  
TrMDHe : AAGGTTCGTCTGGTCGCAGGAGCAGAAGAGATATCAACTTGGTCCCCTTAATGAG : 1080

\* 1100 \* 1120 \* 1140  
TrMDHe : TATGAGAGGATTGGATTAGAAAAAGCGAAGAAAGAGTTAGCAGGAAGCATCCAGAAGGGA : 1140

\* 1160 \* 1180 \* 1200  
TrMDHe : GTAGAATTCAAAAAAAAAAAAAGATAAGGAAAAATTAGTTTGATTGNCTCTTCT : 1200

\* 1220 \*  
TrMDHe : ATATCTATAAAGAACCTTGTGTAAATAATTCC : 1230

Figure 68 Deduced amino acid sequence of TrMDHe

\* 20 \* 40 \* 60  
TrMDHe : MEAHAAGANQRIARIISAHLQPPNFQEGGDVAISKANCRAKGGAPGFVAILGAAGGIGQS : 60

\* 80 \* 100 \* 120  
TrMDHe : LSLLLKINPLVSVLHLYDVVNTPGVTADVSHIDTGAVVRGFLGQAQLENALTGMDLVVIP : 120

\* 140 \* 160 \* 180  
TrMDHe : AGVPRKPGMTRDDLFKINAGIVRTLSEGIAKSCPNAIVNLISNPVNSTVPIAAEVFKKAG : 180

\* 200 \* 220 \* 240  
TrMDHe : TYDPKRLLGVTTLDVVRANTFVAEVLGVDPREVDVPVVGGHAGVTILPLLSQVKPPSSFT : 240

\* 260 \* 280 \* 300  
TrMDHe : AEETEYLTXRRIQXGGTQVVEAKAGAGSATLMAYAAAKFANACLRGLKGEAGIVECAFVDS : 300

\* 320 \* 340 \*  
TrMDHe : QVTELPFFAAKVRLGRGGAEEIYQLGPLNEYERIGLEKAKKELAGSIQKGVEFIKKKR : 359

Figure 69 Nucleotide sequences of nucleic acid fragments contributing to the consensus contig sequence TrMDHe

	*	20	*	40	*	60	
TrMDHe1	:	TTNTNTTATTATGTTTTNCCTCCTACATATAACTCTNACTTNGCATACACTGTG				: 60	
TrMDHe2	:	-				GNG : 3	
TrMDHe3	:	-				GTG : 3	
TrMDHe4	:	-				-	
TrMDHe5	:	-				-	
TrMDHe6	:	-				-	
TrMDHe7	:	-				-	
TrMDHe8	:	-				-	
TrMDHe9	:	-				-	
TrMDHe10	:	-				-	
	*	80	*	100	*	120	
TrMDHe1	:	TCTCT-AATTATTATTAGTCCTTGAAATGGAAGCACATGCAGCTGGTACCAATCAGAGG				: 119	
TrMDHe2	:	TCTCTCAATTATTATTAGTCCTTAGAAAATGGAAGCACATGCAGCTGGTGCCAAATCAGAGG				: 63	
TrMDHe3	:	TCTCTCAATTATTATTAGTCCTTAGAAAATGGAAGCCATGCAGCTGGAGCCAATCAGAGG				: 63	
TrMDHe4	:	-GNAGTCCTTAAATGGAAGCACATGCAGCTGGAGCC-ATC-GAGG				: 44	
TrMDHe5	:	-GAGAAAATGGAAGCACATGCAGCTGGAGCCAATCAGAGG				: 38	
TrMDHe6	:	-CCANTGCAGCTGGTGCCANTNNNGAGG				: 26	
TrMDHe7	:	-				-	
TrMDHe8	:	-				-	
TrMDHe9	:	-				-	
TrMDHe10	:	-				-	
	*	140	*	160	*	180	
TrMDHe1	:	ATTGCAAGAACATCTGCTCATCTTCAAGCCTCCAAATTCCAGGAAGGAGGTGATGTTGCA				: 179	
TrMDHe2	:	ATTGCAAGAACATCTGCTCATCTTCAACCTCCAAATTCCAGGAAGGAGGTGATGTTGCA				: 123	
TrMDHe3	:	ATTGCAAGAACATCTGCTCATCTTCAACCTCCAAATTCCAGGAAGGAGGTGATGTTGCA				: 123	
TrMDHe4	:	ATTGCAAGAACATCTGCTCATCTTC-CCCTCCAAATTCCAGGAAGGAAGGTGATGTTGCA				: 103	
TrMDHe5	:	ATTGCAAGAACATCTGCTCATCTTCAACCTCCAAATTCCAGGAAGGAGGTGATGTTGCA				: 98	
TrMDHe6	:	ATTGCAAGAACATCTGCTCATCTT-NACCTCC-AATTCCAGGAAGGAGGTGATGTTGCA				: 83	
TrMDHe7	:	-				-	
TrMDHe8	:	-				-	
TrMDHe9	:	-				-	
TrMDHe10	:	-				-	
	*	200	*	220	*	240	
TrMDHe1	:	ATTAGCAAAGCTAATGCGAGAGCAAAAGGTGGGGCGCCGGGATTCAAAGTAGCAATCTTG				: 239	
TrMDHe2	:	ATTAGCAAAGCTAATGCGAGAGCAAAAGGTGGGGCGCCGGGATTCAAAGTAGCAATCTTG				: 183	
TrMDHe3	:	ATTAGCAAAGCTAATGCGAGAGCAAAAGGTGGGGCGCCGGGATTCAAAGTAGCAATCTTG				: 183	
TrMDHe4	:	ATTAGCAAAGCTAATGCGAGAGCAAAAGGTGGGGCGCCGGGATTCAAAGTAGCAATCTTG				: 163	
TrMDHe5	:	ATTAGCAAAGCTAATGCGAGAGCAAAAGGTGGGGCGCCGGGATTCAAAGTAGCAATCTTG				: 158	
TrMDHe6	:	ATTAGCAAAGCTAATGCGAGAGCAAAAGGTGGGGCGCCGGGATTCAAAGTAGCAATCTTG				: 143	
TrMDHe7	:	-				-	
TrMDHe8	:	-				-	
TrMDHe9	:	-				-	
TrMDHe10	:	-				-	

	*      260      *	*      280      *	*      300      :
TrMDHe1	: GGGGCTGCTGGTGAATTGGTCAATCCCTTCTTGCTGTTGAAGAATGCAATCCATTGGTT		: 299
TrMDHe2	: GGGGCTGCTGGTGAATTGGTCAATCCCTTCTTGCTGTTGAAGAATGCAATCCATTGGTT		: 243
TrMDHe3	: GGGGCTGCTGGTGAATTGGTCAATCCCTTCTTGCTGTTGAAGAATGCAATCCATTGGTT		: 243
TrMDHe4	: GGGGCTGCTGGTGAATTGGTCAATCCCTTCTTGCTGTTGAAGAATGCAATCCATTGGTT		: 243
TrMDHe5	: GGGGCTGCTGGTGAATTGGTCAATCCCTTCTTGCTGTTGAAGAATGCAATCCATTGGTT		: 223
TrMDHe6	: GGGGCTGCTGGTGAATTGGTCAATCCCTTCTTGCTGTTGAAGAATGCAATCCATTGGTT		: 218
TrMDHe7	: -----		: 203
TrMDHe8	: -----		: -
TrMDHe9	: -----		: -
TrMDHe10	: -----		: -
	*      320      *	*      340      *	*      360      :
TrMDHe1	: TCAGTTCTTCATCTTATGATGTTGTCAACACTCCTGGTCACTGGTGTGATGTTAGTCAC		: 359
TrMDHe2	: TCAGTTCTTCATCTTATGATGTTGTCAACACTCCTGGTCACTGGTGTGATGTTAGTCAC		: 303
TrMDHe3	: TCAGTTCTTCATCTTATGATGTTGTCAACACTCCTGGTCACTGGTGTGATGTTAGTCAC		: 303
TrMDHe4	: TCAGTTCTTCATCTTATGATGTTGTCAACACTCCTGGTCACTGGTGTGATGTTAGTCAC		: 283
TrMDHe5	: TCAGTTCTTCATCTTATGATGTTGTCAACACTCCTGGTCACTGGTGTGATGTTAGTCAC		: 278
TrMDHe6	: TCAGTTCTTCATCTTATGATGTTGTCAACACTCCTGGTCACTGGTGTGATGTTAGTCAC		: 263
TrMDHe7	: -----		: -
TrMDHe8	: -----		: -
TrMDHe9	: -----		: -
TrMDHe10	: -----		: -
	*      380      *	*      400      *	*      420      :
TrMDHe1	: ATTGACACCGGTGCTGTGGTTCTAGGGCAGGCACAACCTGAGAATGCACTT		: 419
TrMDHe2	: ATTGACACCGGTGCTGTGGTTCTAGGGCAGGCACAACCTGAGAATGCACTT		: 363
TrMDHe3	: ATTGACACCGGTGCTGTGGTTCTAGGGCAGGCACAACCTGAGAATGCACTT		: 363
TrMDHe4	: ATTGACACCGGTGCTGTGGTTCTAGGGCAGGCACAACCTGAGAATGCACTT		: 343
TrMDHe5	: ATTGACACCGGTGCTGTGGTTCTAGGGCAGGCACAACCTGAGAATGCACTT		: 338
TrMDHe6	: ATTGACACCGGTGCTGTGGTTCTAGGGCAGGCACAACCTGAGAATGCACTT		: 323
TrMDHe7	: -----		: 22
TrMDHe8	: -----		: -
TrMDHe9	: -----		: -
TrMDHe10	: -----		: -
	*      440      *	*      460      *	*      480      :
TrMDHe1	: ACAGGCATGGACTTGGTCGTTACCTGCTGGTGTGCCGAGGAACCTGGAATGACAAGG		: 479
TrMDHe2	: ACAGGCATGGACTTGGTCGTTACCTGCTGGTGTGCCGAGGAACCTGGAATGACAAGG		: 423
TrMDHe3	: ACAGGCATGGACTTGGTCGTTACCTGCTGGTGTGCCGAGGAACCTGGAATGACAAGG		: 423
TrMDHe4	: ACAGGCATGGACTTGGTCGTTACCTGCTGGTGTGCCGAGGAACCTGGAATGACAAGG		: 403
TrMDHe5	: ACAGGCATGGACTTGGTCGTTACCTGCTGGTGTGCCGAGGAACCTGGAATGACAAGG		: 398
TrMDHe6	: ACAGGCATGGACTTGGTCGTTACCTGCTGGTGTGCCGAGGAACCTGGAATGACAAGG		: 383
TrMDHe7	: ACAGGCATGGACTTGGTCGTTACCTGCTGGTGTGCCGAGGAACCTGGAATGACAAGG		: 82
TrMDHe8	: -----		: -
TrMDHe9	: -----		: -
TrMDHe10	: -----		: -
	*      500      *	*      520      *	*      540      :
TrMDHe1	: GATGACTTATTAAGATAATGCTGGAATTGTGAGGACTCTTAGCGAAGGAATTGCCAAG		: 539
TrMDHe2	: GATGACTTATTAAGATAATGCTGGAATTGTGAGGACTCTTAGCGAAGGAATTGCCAAG		: 483
TrMDHe3	: GATGACTTATTAAGATAATGCTGGAATTGTGAGGACTCTTAGCGAAGGAATTGCCAAG		: 483
TrMDHe4	: GATGACTTATTAAGATAATGCTGGAATTGTGAGGACTCTTAGCGAAGGAATTGCCAAG		: 463
TrMDHe5	: GATGACTTATTAAGATAATGCTGGAATTGTGAGGACTCTTAGCGAAGGAATTGCCAAG		: 458
TrMDHe6	: GATGACTTATTAAGATAATGCTGGAATTGTGAGGACTCTTAGCGAAGGAATTGCCAAG		: 443
TrMDHe7	: GATGACTTATTAAGATAATGCTGGAATTGTGAGGACTCTTAGCGAAGGAATTGCCAAG		: 142
TrMDHe8	: -----		: -
TrMDHe9	: -----		: -
TrMDHe10	: -----		: -

	* 560 *	* 580 *	* 600 *	
TrMDHe1	: AGCTGTCCTAATGCAATTGTCAACTTGATTAGCAATCCAGTGAATTCCACTGTGCCAATT			: 599
TrMDHe2	: AGCTGTCCTAATGCAATTGTCAACTTGATTAGCAATCCAGTGAATTCCACTGTGCCAATT			: 543
TrMDHe3	: AGCTGTCCTAATGCAATTGTCAACTTGATTAGCAATCCAGTGAATTCCACTGTGCCAATT			: 543
TrMDHe4	: AGCTGTCCTAATGCAATTGTCAACTTGATTAGCAATCCAGTGAATTCCACTGTGCCAATT			: 523
TrMDHe5	: AGCTGTCCTAATGCAATTGTCAACTTGATTAGCAATCCAGTGAATTCCACTGTGCCAATT			: 518
TrMDHe6	: AGCTGTCCTAATGCAATTGTCAACTTGATTAGCAATCCAGTGAATTCCACTGTGCCAATT			: 503
TrMDHe7	: AGCTGTCCTAATGCAATTGTCAACTTGATTAGCAATCCAGTGAATTCCACTGTGCCAATT			: 202
TrMDHe8	:			:
TrMDHe9	:			:
TrMDHe10	:			:

	* 620 *	* 640 *	* 660 *	
TrMDHe1	: GCTGCTGAGGTCTTCAAGAAAAGCCGGTACATATGATCCAAAGCGACTTTA <del>GGGT</del> AACA			: 659
TrMDHe2	: GCTGCTGAGGTCTTCAAGAAAAGCCGGTACATATGATCCAAAGCGACTTTA <del>GGGT</del> AACA			: 574
TrMDHe3	: GCTGCTGAGGTCTTCAAGAAAAGCCGGTACATATGATCCAAAGCGACTTTA <del>GGGT</del> AACA			: 576
TrMDHe4	: GCTGCTGAGGTCTTCAAGAAAAGCCGGTACATATGATCCAAAGCGACTTTA <del>GGGT</del> AACA			: 583
TrMDHe5	: GCTGCTGAGGTCTTCAAGAAAAGCCGGTACATATGATCCAAAGCGACTTTA <del>GGGT</del> AACA			: 578
TrMDHe6	: GCTGCTGAGGTCTTCAAGAAAAGCCGGTACATATGATCCAAAGCGACTTTA <del>GGGT</del> AACA			: 555
TrMDHe7	: GCTGCTGAGGTCTTCAAGAAAAGCCGGTACATATGATCCAAAGCGACTTTA <del>GGGT</del> AACA			: 262
TrMDHe8	:			: 28
TrMDHe9	:			:
TrMDHe10	:			:

	* 680 *	* 700 *	* 720 *	
TrMDHe1	: ACCCTCGATGNTGT			: 673
TrMDHe2	:			:
TrMDHe3	:			:
TrMDHe4	: ACCCTCGATG-			:
TrMDHe5	: ACCCTNGATGTTGNGAGGGCAAATACTTTGTGGCANAAG-NCTTGGNGTTGAA <del>CC</del> AAA			: 593
TrMDHe6	:			: 637
TrMDHe7	: ACCCTCGATGTTGAGGGCAAATACTTTGTGGCAGAAGTACTTGATGTTGATCCAAGA			:
TrMDHe8	: ACCCTCGATGTTGAGGGCAAATACTTTGTGGCAGAAGTACTTGATGTTGATCCAAGA			: 322
TrMDHe9	:			:
TrMDHe10	:			: 88

	* 740 *	* 760 *	* 780 *	
TrMDHe1	:			:
TrMDHe2	:			:
TrMDHe3	:			:
TrMDHe4	:			:
TrMDHe5	: NAGGGTNAATNTCCANTGGTAGGAGGGCCCGCNGGANT-ACAANATTACC-CTTTTGT-			: 693
TrMDHe6	:			:
TrMDHe7	: GAGGTTGATGTTCCAGNGTAGGAGGCACGCAGAGT-ACAATATTACCTCTTTGTCA			:
TrMDHe8	: GAGGTTGATGTTCCAGTGTTAGGAGGGCACGCAGGAGTCACAATATTACCTCTTTGTCA			: 381
TrMDHe9	:			:
TrMDHe10	:			: 148

	* 800 *	* 820 *	* 840 *	
TrMDHe1	:			:
TrMDHe2	:			:
TrMDHe3	:			:
TrMDHe4	:			:
TrMDHe5	:			:
TrMDHe6	:			:
TrMDHe7	: CAGGTTAACGCCTNCCAGTA <del>CTT</del> -ACCGNAGAA <del>AA</del> ACCGAATACCTGACANANCNATT			: 440
TrMDHe8	: CAGGTTAACGCCTCCAGTAGCTCAG <del>CT</del> GCAGAAGAAACCGAATACCTGACAAATCGCATT			: 208
TrMDHe9	:			:
TrMDHe10	:			:

	*      860	*      880	*      900	
TrMDHe1	:	- - - - -	- - - - -	:
TrMDHe2	:	- - - - -	- - - - -	:
TrMDHe3	:	- - - - -	- - - - -	:
TrMDHe4	:	- - - - -	- - - - -	:
TrMDHe5	:	- - - - -	- - - - -	:
TrMDHe6	:	- - - - -	- - - - -	:
TrMDHe7	:	CAAAANGCGGAACACAAGTGTGAGGCAAAG	- - - - -	:
TrMDHe8	:	CAAAA <del>TGG</del> GGAACAGAAGTTGTTGAGGCAAAGGCTGGGCTGGTTGGCAACACTANT	A	: 473
TrMDHe9	:	- - - - - GTTGTTGAGGCAAAGGCTGGGCTGGTTGGCAACACTANTN	:	: 268
TrMDHe10	:	- - - - - TTGTTGAGGAAAGGCTGGGCTGGTTGGG-NAC-CT-NTN	:	: 42
	*      920	*      940	*      960	
TrMDHe1	:	- - - - -	- - - - -	:
TrMDHe2	:	- - - - -	- - - - -	:
TrMDHe3	:	- - - - -	- - - - -	:
TrMDHe4	:	- - - - -	- - - - -	:
TrMDHe5	:	- - - - -	- - - - -	:
TrMDHe6	:	- - - - -	- - - - -	:
TrMDHe7	:	- - - - -	- - - - -	:
TrMDHe8	:	ATGGC <del>A</del> TATGCAGCTGCCAAGTTGCTAACGCATGCCTCCGTGGCTTGAAAGGAGAACCC	:	: 328
TrMDHe9	:	ATGGCCTATGCAGCTGCCAAGTTGCTAACGCATGCCTCCGTGGCTTGAAAGGAGAACCC	:	: 102
TrMDHe10	:	ATGGCCTATGCAGCTGCCAAGTTGCTAACGCATGCCTCCGTGGCTTGAAAGGAGAACCC	:	: 97
	*      980	*      1000	*      1020	
TrMDHe1	:	- - - - -	- - - - -	:
TrMDHe2	:	- - - - -	- - - - -	:
TrMDHe3	:	- - - - -	- - - - -	:
TrMDHe4	:	- - - - -	- - - - -	:
TrMDHe5	:	- - - - -	- - - - -	:
TrMDHe6	:	- - - - -	- - - - -	:
TrMDHe7	:	- - - - -	- - - - -	:
TrMDHe8	:	GGGATAGTGGAGTGTGCTTTGTTGATTCTCAGGTTACGGAACCTCCTTCTTCAGCC	:	: 388
TrMDHe9	:	GGGATAGTGGAGTGTGCTTTGTTGATTCTCAGGTTACGGAACCTCCTTCTTCAGCC	:	: 162
TrMDHe10	:	GGGATAGTGGAGTGTGCTTTGTTGATTCTCAGGTTACGGAACCTCCTTCTTCAGCC	:	: 157
	*      1040	*      1060	*      1080	
TrMDHe1	:	- - - - -	- - - - -	:
TrMDHe2	:	- - - - -	- - - - -	:
TrMDHe3	:	- - - - -	- - - - -	:
TrMDHe4	:	- - - - -	- - - - -	:
TrMDHe5	:	- - - - -	- - - - -	:
TrMDHe6	:	- - - - -	- - - - -	:
TrMDHe7	:	- - - - -	- - - - -	:
TrMDHe8	:	AAGGTTCGTCTGGTCGGGTGGAGCAGAAGAGATATA <del>C</del> CAACTTGTCCCCTTAATGAG	:	: 448
TrMDHe9	:	AAGGTTCGTCTGGTCGGGTGGAGCAGAAGAGATATA <del>C</del> CAACTTGTCCCCTTAATGAG	:	: 222
TrMDHe10	:	AAGGTTCGTCTGGTCGGGTGGAGCAGAAGAGATATA <del>C</del> CAACTTGTCCCCTTAATGAG	:	: 217
	*      1100	*      1120	*      1140	
TrMDHe1	:	- - - - -	- - - - -	:
TrMDHe2	:	- - - - -	- - - - -	:
TrMDHe3	:	- - - - -	- - - - -	:
TrMDHe4	:	- - - - -	- - - - -	:
TrMDHe5	:	- - - - -	- - - - -	:
TrMDHe6	:	- - - - -	- - - - -	:
TrMDHe7	:	- - - - -	- - - - -	:
TrMDHe8	:	TATGAGAGGATTGG <del>G</del> TTGAAAAAGCGAAGAA <del>G</del> GAGTTAGC <del>G</del> GGAAAGCATCCAGAAGGG	:	: 508
TrMDHe9	:	TATGAGAGGATTGGATTAGAAAAAGCGAAGAAAGAGTTAGCAGGAAGCATCCAGAAGGG	:	: 282
TrMDHe10	:	TATGAGAGGATTGGATTAGAAAAAGCGAAGAAAGAGTTAGCAGGAAGCATCCAGAAGGG	:	: 277

	*	1160	*	1180	*	1200	
TrMDHe1	:	-	-	-	-	-	-
TrMDHe2	:	-	-	-	-	-	-
TrMDHe3	:	-	-	-	-	-	-
TrMDHe4	:	-	-	-	-	-	-
TrMDHe5	:	-	-	-	-	-	-
TrMDHe6	:	-	-	-	-	-	-
TrMDHe7	:	-	-	-	-	-	-
TrMDHe8	:	GTAGAATTCATCA <del>GAAAAA</del> AAGTGAGATAAGGAAAATTAGTTTGTATTGNCTCTTCT				568	
TrMDHe9	:	GTAGAATTCATCA <del>G</del> <u>A</u> AAAAAANAA-				306	
TrMDHe10	:	GTAGAATTCATCAAAAAAAAAN-				299	

	*	1220	*	
TrMDHe1	:	-	-	-
TrMDHe2	:	-	-	-
TrMDHe3	:	-	-	-
TrMDHe4	:	-	-	-
TrMDHe5	:	-	-	-
TrMDHe6	:	-	-	-
TrMDHe7	:	-	-	-
TrMDHe8	:	ATATCTATAAAGAACTTGTGTAATAATTCC	598	
TrMDHe9	:	-	-	-
TrMDHe10	:	-	-	-

Figure 70 Consensus contig nucleotide sequence of TrMDHf

\* 20 \* 40 \* 60  
TrMDHf : GNNTACNGCTATCNACCCTTTCTTATAACAATAATNATAGATAAAATTCACTGCTAAA : 60

\* 80 \* 100 \* 120  
TrMDHf : TTATGGAGCCAAATTCAAGATGCAAATCAACGAATCGCAAGAATCTCCGCCACCTAAATC : 120

\* 140 \* 160 \* 180  
TrMDHf : CTCCAATTCAAGATGAACATGGTGATTCTTCTTGACAAGTTCCATTGCCGTG : 180

\* 200 \* 220 \* 240  
TrMDHf : CAAAAGGTGGAGCACCTGGATTCAAAGTTGCAATTAGGTGCTGCTGGCATAGGTC : 240

\* 260 \* 280 \* 300  
TrMDHf : AACCTCTTCAATGTTGATGAAGATGAATCCTTGGTTNAGTCTTCATCTTATGATG : 300

\* 320 \* 340 \* 360  
TrMDHf : TTGTTAATACTCCTGGTGTACTTCTGATATTAGTCATATGGATACTGCTGCTGGTTC : 360

\* 380 \* 400 \* 420  
TrMDHf : GAGGGTTTTGGGGCAAAATCAGCTTGAGGATGCACTTACAGGTATGGATTGGTAATCA : 420

\* 440 \* 460 \* 480  
TrMDHf : TTCCTGCCGGTGTCCCCGTAACCTGGAATGACAAGAGATGATCTCTCAATATAATG : 480

\* 500 \* 520 \* 540  
TrMDHf : CCGGGATCGTTAACACTCTGTGAAGCAATTGCAAAGCGATGTCCTAAGGCATTGTCA : 540

\* 560 \* 580 \* 600  
TrMDHf : ACGTGATTAGTAATCCGGTTAACCTCCACTGTCCCCATTGCGGCTGAAGTTTCAAAAGAG : 600

\* 620 \* 640 \* 660  
TrMDHf : CCGGTACTTATGATCCCAAGAGACTTTGGGAGTGACAATGCTTGTGGATGTCGGTCC : 660

\* 680 \* 700 \* 720  
TrMDHf : ATACGTTGTGGCTGAAGTTCTTGGTCTTGTGATCCAAGGGATGTGGATGTCAGTTGTCG : 720

\* 740 \* 760 \* 780  
TrMDHf : GAGGACATGCCGGAATCACCATTTACCTCTGCTTCTCAGGTTAACCCACATTCCCTTT : 780

\* 800 \* 820 \* 840  
TrMDHf : TCACGACAAAGGAAATTGAGTACTTGACAGATCGCATAACAAACGGTGGAACTGAAGTTG : 840

\* 860  
TrMDHf : TTGAGGCCAAAGCTGGAGCTGGCTCT : 866

Figure 71 Deduced amino acid sequence of TrMDHf

\* 20 \* 40 \* 60  
TrMDHf : MEPNSDANQRARIARISGHLPNPPNFKMNEHGDSLTSFHCRAKGGAPGFKVAILGAAGGGIGQ : 60

\* 80 \* 100 \* 120  
TrMDHf : PLSMLMKMNPLVXVLHLYDVVNTPGVTSDISHMDTAAVVRGFLGQNQLEDALTGMDLVII : 120

\* 140 \* 160 \* 180  
TrMDHf : PAGVPRKPGMTRDDLFNINAGIVKTLCEAIAKRCPKAIVNVISNPVNSTVPIAAEVFKRA : 180

\* 200 \* 220 \* 240  
TrMDHf : GTYDPKRLLGVTMLDVVRANTFVAEVLGLDPRDVPVVGGHAGITILPLSQVKPHSSF : 240

\* 260  
TrMDHf : TTKEIEYLTDRIQNGGTEVVEAKAGAGS : 268

Figure 72 Nucleotide sequences of nucleic acid fragments contributing to the consensus contig sequence TrMDHf

TrMDHf1 :	GNNTACNGCTATCNACCCTCTTCCTTACAAATAATNATAGATAAATTCTCATCTGCTAAA	* 20 * 40 * 60	: 60
TrMDHf2 :	-----		
TrMDHf3 :	-----		
TrMDHf1 :	TTATGGAGCCAATTCAAGATGAAACATGGTGATTCTTCTTGACAAGTTCCATTGCCGTG	* 80 * 100 * 120	: 120
TrMDHf2 :	-----		
TrMDHf3 :	-----		
TrMDHf1 :	CTCCCATTCAAGATGAAACATGGTGATTCTTCTTGACAAGTTCCATTGCCGTG	* 140 * 160 * 180	: 180
TrMDHf2 :	-----		
TrMDHf3 :	-----		
TrMDHf1 :	CAAAAGGTGGAGCACCTGGATTCAAAGTTGCAATTAGGTGCTGCTGGCATAGGTC	* 200 * 220 * 240	: 240
TrMDHf2 :	-----		
TrMDHf3 :	-----		
TrMDHf1 :	AACCTCTTCAATGTTGAAAGATGAATCCATTGGTTT-AGTTCTCATCTTATGATG	* 260 * 280 * 300	: 299
TrMDHf2 :	ACCTCTT-NATGTTGAAAGATGAATCCTATGGTTT-AGTTCTCATCTTATGATG		: 70
TrMDHf3 :	-----		
TrMDHf1 :	TTGTTAATACTCCTGGTTACTTCTGATATTAGTCAGATGGATACTGGTGCTGTTGTT	* 320 * 340 * 360	: 359
TrMDHf2 :	TTGTTAATACTCCTGGTTACTTCTGATATTAGTCAGATGGATACTGGTGCTGTTGTT		: 130
TrMDHf3 :	TTG-TAATACTCCTGGTG-TACTTCTGATATTAGT-ATATGGATACTGGTGCTGTTGTT		: 86
TrMDHf1 :	GAGGATTGGGGAAAATCAGCTGAGGATGCACTTACAGGTATGGATTGGTAATCA	* 380 * 400 * 420	: 419
TrMDHf2 :	GAGGGTTTGGGGAAAATCAGCTGAGGATGCACTTACAGGTATGGATTGGTAATCA		: 190
TrMDHf3 :	GAGGGTTTGGGGAAAATCAGCTGAGGATGCACTTACAGGTATGGATTGGTAATCA		: 146
TrMDHf1 :	TTCCCTGCCTGGTCCCCGTAACCTGGAATGACAAGAGATGATCTCTTCAAATATAATG	* 440 * 460 * 480	: 479
TrMDHf2 :	TTCCCTGCCGGTCCCCGTAACCTGGAATGACAAGAGATGATCTCTTCAAATATAATG		: 250
TrMDHf3 :	TTCCCTGCCGGTCCCCGTAACCTGGAATGACAAGAGATGATCTCTTCAAATATAATG		: 206
TrMDHf1 :	CCGGGATCGTAAACACTCTGTGAAGCAATTGCAGAGCGATGTCTAACGGCGATTGTCA	* 500 * 520 * 540	: 539
TrMDHf2 :	CCGGGATCGTAAACACTCTGTGAAGCAATTGCAAGCGATGTCTAACGGCGATTGTCA		: 310
TrMDHf3 :	CCGGGATCGTAAACACTCTGTGAAGCAATTGCAAGCGATGTCTAACGGCGATTGTCA		: 266
TrMDHf1 :	ACGTGATTAGTAATCGGTTAACCTCCACTGTCC	* 560 * 580 * 600	: 572
TrMDHf2 :	ACGTGATTAGTAATCGGTTAACCTCCACTGTCCCCATTGGCGCTGAAGTTTCAAAAGAG		: 370
TrMDHf3 :	ACGTGATTAGTAATCGGTTAACCTCCACTGTCCCCATTGGCGCTGAAGTTTCAAAAGAG		: 326

\* 620 \* 640 \* 660  
TrMDHf1 : -----  
TrMDHf2 : CCGGTACTTATGATCCCAGAGACTTTGGGAGTGACAATGCTGATGTGGTCGGGCCA : 430  
TrMDHf3 : CCGGTACTTATGATCCCAGAGACTTTGGGAGTGACAATGCTGATGTGGTCGGGCCA : 386

\* 680 \* 700 \* 720  
TrMDHf1 : -----  
TrMDHf2 : ATACGTTGGCTGAAGTTCTGGTCTTGATCCAAGGGATGTGGATGTCCCAGTTGTCG : 490  
TrMDHf3 : ATACGTTGGCTGAAGTTCTGGTCTTGATCCAAGGGATGTGGATGTCCCAGTTGTCG : 446

\* 740 \* 760 \* 780  
TrMDHf1 : -----  
TrMDHf2 : GAGGACATGCCGGAATCACCAATTACCTCTGCTTCTCAGGTTAAACCACATTCCTCTT : 550  
TrMDHf3 : GAGGACATGCCGGAATCACCAATTACCTCTGCTTCTCAGGTTAAACCACATTCCTCTT : 506

\* 800 \* 820 \* 840  
TrMDHf1 : -----  
TrMDHf2 : TCACGACAAAGGAAATTGAGTACTTG----- : 576  
TrMDHf3 : TCACGACAAAGGAAATTGAGTACTTGACAGATCGCATACAAACGGTGGAACTGAAGTTG : 566

\* 860  
TrMDHf1 : -----  
TrMDHf2 : -----  
TrMDHf3 : TTGAGGCCAAGCTGGAGCTGGCTCT : 592

Figure 73 Consensus contig nucleotide sequence of TrMDhg

\* 20 \* 40 \* 60  
TrMDhg : GTAGGCAGCATCTAACAGCACAATGAACATGGAAATGTTGCTTGAAATTATGGACAA : 60

\* 80 \* 100 \* 120  
TrMDhg : TACGGTCCTTAAAAAATCTGTTCTGTTTATTTGTACTTTTTGTTGGAAGATCGT : 120

\* 140 \* 160 \* 180  
TrMDhg : TAGATACATGTGTGGTCTCTCAAAGTTGATAAGGAACCAGTCACTGTATTGGTCAGTGG : 180

\* 200 \* 220 \* 240  
TrMDhg : TGCTGCAGGACAAATTGGNTATGCTCTGNTCCAATGATTGCAAGAGGGATGATGCTAGG : 240

\* 260 \* 280 \* 300  
TrMDhg : CCCAAATCAACCTGGAATTCTTCATATGCTNGATATTGAACCAGGATTAGAGGCCCTAA : 300

\* 320 \* 340 \* 360  
TrMDhg : AGGGGTGAAGATGGAACGTGATTGATGGTCTTCCACTCTTAGAGGTGTTGCTAC : 360

\* 380 \* 400 \* 420  
TrMDhg : TACGGATGTTGTTGAAGCATGCAAGGATGTTAACATTGCTGTTATGCTTGGATCCCC : 420

\* 440 \* 460 \* 480  
TrMDhg : AAGGAAGGAAGGAATGGAAAGAAAAGATGTAATGCTAAGAATGTTCAATTACAAGGC : 480

\* 500 \* 520 \* 540  
TrMDhg : TCAAGCTTCAGCTTGGAGGAGCATGCTGCTGCAGATTGTAAGTGCTAGTGGTAGCCAA : 540

\* 560 \* 580 \*  
TrMDhg : TCCAGCAAACACAAATGCTCTAATATTGAAAGAATTGCTCCATCAATCCCTGAGAAAA : 599

Figure 74 Deduced amino acid sequence of TrMDHg

\* 20 \* 40 \* 60  
TrMDhg : MCGLLKVDKEPVTVLVTGAAGQIXYALXPMIARGMMLGPNQPGILHMXDIEPGLEALKGV : 60

\* 80 \* 100 \* 120  
TrMDhg : KMELIDGAFPLLRGVVATTDVVEACKDVNIAVMLGGSPRKEGMERKDVM SKNVSIYKAQA : 120

\* 140 \*  
TrMDhg : SALEEHAAADCKVLVVANPANTNALILKEFAPSipek : 157

Figure 75 Nucleotide sequences of nucleic acid fragments contributing to the consensus contig sequence TrMDHg

TrMDHg1 :	<b>GTAGGCATCA</b>	* ~20 *	* 40 *	* 60	
TrMDHg2 :	-----	<b>GNNGGATCTAACAG</b>	<b>ACAATGAACATGGAAATGTTGCTTGAAATTATGGACAATA</b>		: 60 : 57
TrMDHg1 :	<b>CGGTCC</b>	* 80 *	* 100 *	* 120	
TrMDHg2 :	<b>CGGTCC</b>	<b>TTAAAAAATCTGTTCTGTTTATTTGTACTTTTGTT</b>	<b>TGGAAGATCGTTAGA</b>		: 122 : 119
TrMDHg1 :	<b>TACATGTGTGGTCTTCTCAAAGTTGATAAGGAACCAGTC</b>	* 140 *	* 160 *	* 180	
TrMDHg2 :	<b>TACATGTGTGGTCTTCTCAAAGTTGATAAGGAACCAGTC</b>	<b>ACTGTATTGGTC</b>	<b>ACTGGTGCTGC</b>		: 184 : 181
TrMDHg1 :	<b>AGGACAAAATTGGNTATGCTCTGN</b>	* 200 *	* 220 *	* 240	
TrMDHg2 :	<b>AGGACAAAATTGG</b>	<b>GTATGCTCTG</b>	<b>TCATGATTGCAAGAGGGATGATGCTAGGCC</b>		: 246 : 243
TrMDHg1 :	<b>MACCTGGNATTG</b>	* 260 *	* 280 *	* 300 *	
TrMDHg2 :	<b>AACCTG</b>	<b>ATTCTCATATGCT</b>	<b>GATATTGAACCAGGATTAGAGGCC</b>		: 276 : 305
TrMDHg1 :	-----	* 320 *	* 340 *	* 360 *	
TrMDHg2 :	<b>ATGGA</b>	<b>ACTGATTGATGGTGC</b>	<b>TTCCCACCTCTTAGAGGTGTTGCTACTACGGATGTTG</b>		: 367
TrMDHg1 :	-----	* 380 *	* 400 *	* 420 *	
TrMDHg2 :	<b>TGAAGC</b>	<b>ATGCAAGGATGTTAACATTGCTGTTATGCTTGGGATCCC</b>			: 429
TrMDHg1 :	-----	* 440 *	* 460 *	* 480 *	
TrMDHg2 :	<b>TGGAAAGAAAAGATGTAATGCTAAGAATGTTCAATT</b>	<b>ACAAGGCT</b>	<b>CAAGCTTCAGCTTG</b>		: 491
TrMDHg1 :	-----	* 500 *	* 520 *	* 540 *	* 5
TrMDHg2 :	<b>GAGGAGCATGCTGCTGCAGATTG</b>	<b>AAAGTGCTAGTGGTAGCCAATCC</b>	<b>AGCAAACACAAATGC</b>		: 553
TrMDHg1 :	-----	* 60 *	* 580 *		
TrMDHg2 :	<b>TCTAATATTGAAAGAATTGCTCCATCAATCCCTGAGAAA</b>				: 594

Figure 76 Consensus contig nucleotide sequence of TrMDHh

\* 20 \* 40 \* 60  
TrMDHh : GNNTACNGCTATCNACCCTCTTCTTATAACAATAATNATAGATAAAATTCATCTGCTAAA : 60

\* 80 \* 100 \* 120  
TrMDHh : TTATGGAGCCAAATTCAAGATGCAAATCAACGAATCGCAAGAATCTCCGGCACCTAAATC : 120

\* 140 \* 160 \* 180  
TrMDHh : CTCCCATTCAAGATGAACATGGATTCTCTTGACAAGTTCCATTGCCGTG : 180

\* 200 \* 220 \* 240  
TrMDHh : CAAAAGGTGGAGCACCTGGATTCAAAGTTGCAATTAGGTGCTGCTGGGGCATAGGTC : 240

\* 260 \* 280 \* 300  
TrMDHh : AACCTCTTCAATGTTGATGAAGATGAATCCTTGGTTNAGTTCTTCATTTATGATG : 300

\* 320 \* 340 \* 360  
TrMDHh : TTGTTAATACTCCTGGTGTACTTCTGATATTAGTCATATGGATACTGCTGCTGTTGTC : 360

\* 380 \* 400 \* 420  
TrMDHh : GAGGGTTTTGGGGCAAAATCAGCTTGAGGATGCACCTACAGGTATGGATTGGTAATCA : 420

\* 440 \* 460 \* 480  
TrMDHh : TTCCTGCCGGTGTCCCCGTAAACCTGGAATGACAAGAGAGATGATCTCTCAATATAATG : 480

\* 500 \* 520 \* 540  
TrMDHh : CCGGGATCGTAAACACTCTGTGAAGCAATTGCAAAGCGATGTCCTAACCGCGATTGTCA : 540

\* 560 \* 580 \* 600  
TrMDHh : ACGTGATTAGTAATCCGGTTAACTCCACTGTCCCCATTGCGGCTGAAGTTTCAAAAGAG : 600

\* 620 \* 640 \* 660  
TrMDHh : CCGGTACTTATGATCCCAAGAGAGCTTGGGAGTGACAATGCTTGATGTGGTTGGGCCA : 660

\* 680 \* 700 \* 720  
TrMDHh : ATACGTTGTGGCTGAAGTTCTGGTCTTGATCCAAGGGATGTGGATGTCCCAGTTGTCG : 720

\* 740 \* 760 \* 780  
TrMDHh : GAGGACATGCCGGAATCACCATTACCTCTGCTTCTCAGGTTAAACCACATTCTCTT : 780

\* 800 \* 820 \* 840  
TrMDHh : TCACGACAAAGGAAATTGAGTACTTGACAGATCGCATAACAAACGGTGGAACTGAAGTTG : 840

\* 860  
TrMDHh : TTGAGGCCAAAGCTGGAGCTGGCTCT : 866

Figure 77 Deduced amino acid sequence of TrMDH<sub>h</sub>

\* 20 \* 40 \* 60  
TrMDH<sub>h</sub> : MEPNSDANQRIARISGHLNPPNFKMNEHGDSLTSFHCRAGGAPGFKVAILGAAGGGIGQ : 60

\* 80 \* 100 \* 120  
TrMDH<sub>h</sub> : PLSMLMKMNPLVXVLHLYDVVNTPGVTS DISHMDTA AVVRGFLGQNQLEDALTGMDLVII : 120

\* 140 \* 160 \* 180  
TrMDH<sub>h</sub> : PAGVPRKPGMTRDDL FNINAGIVKTLCEAI AKRCPKAIVNVISNPVNSTVPIAAEVFKRA : 180

\* 200 \* 220 \* 240  
TrMDH<sub>h</sub> : GTYDPKRLLGVMTLDVV RANTFVAEV LGIDPRDV DV PVVG GHAGIT I LPLL SQVKPHSSF : 240

\* 260  
TrMDH<sub>h</sub> : TTKEIEYLTDRIQNGGTEVVEAKAGAGS : 268

Figure 78 Nucleotide sequences of nucleic acid fragments contributing to the consensus contig sequence TrMDHh

TrMDHh1 :	* 20 * 40 * 60				
TrMDHh2 :	<del>GNNTACNGCTATCNACCCTTCTTCCTTATAACATAATNATAGATAAAATTCACTGCTAAA</del>				: 60
TrMDHh3 :	<del>- - - - -</del>				: -
TrMDHh1 :	* 80 * 100 * 120				
TrMDHh2 :	<del>TTATGGAGCCAAATTCAAGATGCAAATCAACGAATCGCAAGAATCTCCGCCACCTAAATC</del>				: 120
TrMDHh3 :	<del>- - - - -</del>				: -
TrMDHh1 :	* 140 * 160 * 180				
TrMDHh2 :	<del>CTCCCCAATTCAAGATGAATGAACATGGTATTCTCTTGACAAGTTTCCATTGCCGTG</del>				: 180
TrMDHh3 :	<del>- - - - -</del>				: -
TrMDHh1 :	* 200 * 220 * 240				
TrMDHh2 :	<del>CAAAAGGTGGAGCACCTGGATTCAAAGTTGCAATTAGGTGCTGCTGGCATAGGTC</del>				: 240
TrMDHh3 :	<del>- - - - -</del>				: 12
TrMDHh1 :	* 260 * 280 * 300				
TrMDHh2 :	<del>AACCTCTTCAATGTTGATGAAGATGAATCCCTGGTTT</del>	<del>AGTTCTTGTATCTTATGATG</del>			: 299
TrMDHh3 :	<del>AACCTCTT</del>	<del>NATGTTGATGAAGATGAATCCCTGGTTT</del>	<del>AGTTCTTGTATCTTATGATG</del>		: 70
	<del>TTGGTTTNN</del>	<del>GTTCTTATNCTTATGATG</del>			: 29
TrMDHh1 :	* 320 * 340 * 360				
TrMDHh2 :	<del>TTGTTAAACTCTGGTGTACTTCTGATATTAGTCAGCTGAGATGCTGCTGTTGTT</del>				: 359
TrMDHh3 :	<del>TTG</del>	<del>TAATGTTGATCTGGTGTACTTCTGATATTAGTCAGCTGAGATGCTGCTGTTGTT</del>			: 86
TrMDHh1 :	* 380 * 400 * 420				
TrMDHh2 :	<del>GAGGGTTTTGGGGCAAAATCAGCTTGAGGATGCACCTACAGGTATGGATTGTAATCA</del>				: 419
TrMDHh3 :	<del>GAGGGTTTTGGGGCAAAATCAGCTTGAGGATGCACCTACAGGTATGGATTGTAATCA</del>				: 190
	<del>GAGGGTTTTGGGGCAAAATCAGCTTGAGGATGCACCTACAGGTATGGATTGTAATCA</del>				: 146
TrMDHh1 :	* 440 * 460 * 480				
TrMDHh2 :	<del>TTCCTGCTGGTGTCCCCGTAACCTGGAAATGACAAGAGATGATCTCTTC</del>	<del>CAATATAATG</del>			: 479
TrMDHh3 :	<del>TTCCTGCCGGTGTCCCCGTAACCTGGAAATGACAAGAGATGATCTCTTC</del>	<del>CAATATAATG</del>			: 250
	<del>TTCCTGCCGGTGTCCCCGTAACCTGGAAATGACAAGAGATGATCTCTTC</del>	<del>CAATATAATG</del>			: 206
TrMDHh1 :	* 500 * 520 * 540				
TrMDHh2 :	<del>CCGGGATCGTTAACACACTCTGTGAAGCAATTGC</del>	<del>AAAGCGATGTCCTAAGCGATTGTCA</del>			: 539
TrMDHh3 :	<del>CCGGGATCGTTAACACACTCTGTGAAGCAATTGCAAAAGCGATGTCCTAAGCGATTGTCA</del>				: 310
	<del>CCGGGATCGTTAACACACTCTGTGAAGCAATTGCAAAAGCGATGTCCTAAGCGATTGTCA</del>				: 266
TrMDHh1 :	* 560 * 580 * 600				
TrMDHh2 :	<del>ACGTGATTAGTAATCCGGTTAACCTCCACTGTCC</del>				: 572
TrMDHh3 :	<del>ACGTGATTAGTAATCCGGTTAACCTCCACTGTCC</del>	<del>ATTGCGGCTGAAGTTTCAAAAGAG</del>			: 370
	<del>ACGTGATTAGTAATCCGGTTAACCTCCACTGTCC</del>	<del>ATTGCGGCTGAAGTTTCAAAAGAG</del>			: 326

	* 620		* 640		* 660	
TrMDHh1	:	-----				:
TrMDHh2	:	CCGGTACTTATGATCCCAAGAGACTTTGGGAGTGACAATGCTGATGTGGTCGGGCCA				: 430
TrMDHh3	:	CCGGTACTTATGATCCCAAGAGACTTTGGGAGTGACAATGCTGATGTGGTCGGGCCA				: 386
	* 680		* 700		* 720	
TrMDHh1	:	-----				:
TrMDHh2	:	ATACGTTGGCTGAAGTTCTGGTCTTGATCCAAGGGATGTGGATGTCCCAGTTGTCG				: 490
TrMDHh3	:	ATACGTTGGCTGAAGTTCTGGTCTTGATCCAAGGGATGTGGATGTCCCAGTTGTCG				: 446
	* 740		* 760		* 780	
TrMDHh1	:	-----				:
TrMDHh2	:	GAGGACATGCCGGAATCACCATTTACCTCTGCTTCTCAGGTTAAACACATTCTCTT				: 550
TrMDHh3	:	GAGGACATGCCGGAATCACCATTTACCTCTGCTTCTCAGGTTAAACACATTCTCTT				: 506
	* 800		* 820		* 840	
TrMDHh1	:	-----				:
TrMDHh2	:	TCACGACAAAGGAAATTGAGTACTTG				: 576
TrMDHh3	:	TCACGACAAAGGAAATTGAGTACTTGACAGATCGCATACAAAACGGTGGAACTGAAGTTG				: 566
	* 860					
TrMDHh1	:	-----	:	:	:	
TrMDHh2	:	-----	:	:	:	
TrMDHh3	:	TTGAGGCCAAAGCTGGAGCTGGCTCT	:	592		

Figure 79 Consensus contig nucleotide sequence of TrMDHi

\* 20 \* 40 \* 60  
TrMDHi : GNAATCCTCTTGNCCTCCCTACCCCTCTTTTCTCCTTACACCTCTCTTA : 60

\* 80 \* 100 \* 120  
TrMDHi : TCAACTTCCACCTCTGAACAAAATTCAATCTTCTCATTTCTTACCCCTTTACA : 120

\* 140 \* 160 \* 180  
TrMDHi : AACTTCTTCATAAAGTGTAGGTTTTTATTACTCTTCAAGAACCAACAAACAG : 180

\* 200 \* 220 \* 240  
TrMDHi : TGTTTCTTGAATTCTTGGAAATTTTTCTGCACCAGGCCTGGCACACTTAAA : 240

\* 260 \* 280 \* 300  
TrMDHi : CAACCCCACCTGCTCAAAAATCAACTTCACTCATCACAACTCTCATTCTCTCTAGGAC : 300

\* 320 \* 340 \* 360  
TrMDHi : TCTCCCTAGGCAATATCACTGTACTTTGCACCACTTCACAGAACTCAACATGGCAGAAT : 360

\* 380 \* 400 \* 420  
TrMDHi : TACTTGTCTGTCACCAAATCAAGTGCAGGCTCCAGCTGTACAATCACAGGATCCAA : 420

\* 440 \* 460 \* 480  
TrMDHi : GAATAAGCCTGATTGCTATGGTGTCTGCCTTACCTATGATTGAAGGCTGAAGAGGA : 480

\* 500 \* 520 \* 540  
TrMDHi : GACAAAATCCTGGAAGAAATTAAATCAACATTGCAGTCTCAGGTGCTGCTGGAATGATTTC : 540

\* 560 \* 580 \* 600  
TrMDHi : CAATCATCTACTTTCAAGCTTGCATCTGGTGAAGTTTGGCCAAATCAACCTATTGC : 600

\* 620 \* 640  
TrMDHi : GCTGAAATTATTAGGATCAGAAAGGTCTTCCAAGCTTGAAGGTG : 647

Figure 80 Deduced amino acid sequence of TrMDHi

\* 20 \* 40 \* 60  
TrMDHi : MALAHLNNPTCSKTQLHSSQLSFLSRTLPRQYHCTFAPLHRTQHGRITCSVAPNQVQAPA : 60

\* 80 \* 100 \* 120  
TrMDHi : VQSQDPKNKPDCYGVFCCLTYDLKAEETKSWKKLINIAVSGAAGMISNHLLFKLASGEVF : 120

\* 140  
TrMDHi : GPNQPIALKLLGSERSFQALEG : 142

Figure 81 Nucleotide sequences of nucleic acid fragments contributing to the consensus contig sequence TrMDHi

	*            20            *	*            40            *	*            60	
TrMDHi1 :	GNAATCCTCTTGNCCTCCCCTACCCCTCCTTTCTCCTTCTTACA	-CTTCTCTTC	: 60	
TrMDHi2 :	-----TTCTTAGACCTCTCTTAT		: 19	
	*            80            *	*            100            *	*            120	
TrMDHi1 :	CAACTTTCCACCTCTGAACAAAACCTTC	ATCTTTCTCATTTCTTATACCCTTTAGAAA	: 121	
TrMDHi2 :	-AACTTTCNACCTCTGAACAAA	TT-AATCTTTCT-ATTTCTTATACCCTTTACAAA	: 76	
	*            140            *	*            160            *	*            180	
TrMDHi1 :	CTTCTTCATAAAAGTGT	TATTTTATTACTCTTTCAAGAA	GACAAAAAACAGTGT	: 180
TrMDHi2 :	CTTCTTCATAAAAGTGT	GGGTTTTTTTATTACTCTTTCAAGAAC	GACAAAAAACAGTGT	: 137
	*            200            *	*            220            *	*            240	
TrMDHi1 :	TTCTTGAATTCTTTG	AAATTTTTTTCTGC	AACCATGGCCTTGGGACAGCTTAAACAA	: 241
TrMDHi2 :	TTCTTGAATTCTTGGAA	TTTTTTTTCTGC	AACCATGGCCTTGGGACACTTAAACAA	: 196
	*            260            *	*            280            *	*            300	
TrMDHi1 :	CCCACTTGCTAAAAACTCAACTTC	ACTCATCACAACTCTCATT	TTCTCTAGGACTCTCC	: 302
TrMDHi2 :	CCCACTTGCTAAAAACTCAACTTC	ATTCTCATCACAA	CTCTCATTCTCTAGGACTCTCC	: 257
	*            320            *	*            340            *	*            360	
TrMDHi1 :	CTAGGCAATATCACTGT	ACTTTGCACCAACTTC	CACAGAACTCAACATGGCAGAATTACTTG	: 363
TrMDHi2 :	CTAGGCAATATCACTGT	ACTTTGCACCAACTTC	CACAGAACTCAACATGGCAGAATTACTTG	: 318
	*            380            *	*            400            *	*            420	
TrMDHi1 :	TTCTGTTGCACCAAATCAAGTGCAGGCTCCAGCTGT	ACAATCACAGGATCCCAAGAATAAG	: 424	
TrMDHi2 :	TTCTGTTGCACCAAATCAAGTGCAGGCTCCAGCTGT	ACAATCACAGGATCCCAAGAATAAG	: 379	
	*            440            *	*            460            *	*            480	
TrMDHi1 :	CCTGATTGCTATGGTGT	CTTCTGCCTTACCTATG	ATTGAAAGGCTGAAAGAGGAGACAAAAT	: 485
TrMDHi2 :	CCTGATTGCTATGGTGT	CTTCTGCCTTACCTATG	ATTGAAAGGCTGAAAGAGGAGACAAAAT	: 440
	*            500            *	*            520            *	*            540	
TrMDHi1 :	CCTGGAAAGAAATTAA	ATCAACATTGCAGTCTCAGGTGCTG	GAATGATTCCAATCATCT	: 546
TrMDHi2 :	CCTGGAAAGAAATTAA	ATCAACATTGCAGTCTCAGGTGCTG	GAATGATTCCAATCATCT	: 501
	*            560            *	*            580            *	*            600            *	
TrMDHi1 :	ACTTTCAAGCTTGC	ATCTGGTGAAGTTTG	GGCTCCAAATCAACCTATTGCGCTGA	----- : 602
TrMDHi2 :	ACTTTCAAGCTTGC	ATCTGGTGAAGTTTG	GGGCCAAATCAACCTATTGCGCTGAAATT	: 562
	*            620            *	*            640		
TrMDHi1 :	-----		: -	
TrMDHi2 :	TTAGGATCAGAAAGGT	CCTTCCAAGCTCTGAAGGTG	: 599	

Figure 82 Nucleotide sequence of TrMDHj

\* 20 \* 40 \* 60  
TrMDHj : GCAAAGCNCTNCNGACCTGGTGTGGAGCGAGCAGCTTGCTAGACATAATGGGCAGAT : 60

\* 80 \* 100 \* 120  
TrMDHj : TTTTGCAGGAGCAGGGAAAAGCTCTAAATGCAGTCGCATCTCGCAATGTCAGTTATAGT : 120

\* 140 \* 160 \* 180  
TrMDHj : TGTGGGAAACCCTTGCATACAAATGCATTAATATGCTTGAAGAACGCTCCAAATATTCC : 180

\* 200 \* 220 \* 240  
TrMDHj : TGCAAAAAATTTCATGCTTAACCCGTTAGATGAGAACAGAGCAAAATGTCAGCTAGC : 240

\* 260 \* 280 \* 300  
TrMDHj : CCTCAAGGCAGGTGTCTTCTACGATAAAGTGTGAAATATGACGATATGGGAAACCACTC : 300

\* 320 \* 340 \* 360  
TrMDHj : AACTACTCAGGTCCCCGATTCTAAATGCCAGAACGATGGTTGCCTGTCAAAGAAAGT : 360

\* 380 \* 400 \* 420  
TrMDHj : GATTAAGGATCAAAAGTGGTTAGAGGAAGAGTTCACCGAAAAAGTTCAAAAGAGAGGTGG : 420

\* 440 \* 460 \* 480  
TrMDHj : CGTGCTTATTCAAAAGTGGGAAGATCGTCTGCTGCATCAACTCTGTGTCGATAGTTGA : 480

\* 500 \* 520 \* 540  
TrMDHj : TGCCATACGATCTTGATCACTCCTACTCCGGAGGGTGATTGGTTCTACTGGTGTGTA : 540

\* 560  
TrMDHj : TACAGCTGGAAATCCTTATGGAATAGCTG : 569

Figure 83 Deduced amino acid sequence of TrMDHj

\* 20 \* 40 \* 60  
TrMDHj : QSXXXPGVERAALLDINGQIFAEQGKALNAVASRNVKIVVGNPCNTNALICLKNAPNIP : 60

\* 80 \* 100 \* 120  
TrMDHj : AKNFHALLTRLDENRAKCQLALKAGVFYDKVSNMTIWGNHSTTQVPDFILNARIDGLPVKEV : 120

\* 140 \* 160 \* 180  
TrMDHj : IKDQKWLEEEFTEKVQKRGGVLIQKWGRSSAASTSIVDAIRSLITPTPEGDWFSSTGVY : 180

TrMDHj : TAGNPYGIA : 189

Figure 84 Nucleotide sequence of TrMDHk

\* 20 \* 40 \* 60  
TrMDHk : GNGTAGAACCGTGAAGCCTTTCCCTCCGGTCTCCCCGCTTGCGCCGTGCGCGTCAATT : 60

\* 80 \* 100 \* 120  
TrMDHk : GCTGCTTGTGTCGCGCCTCCAGCTCCTCCTCCACTGTGCCAACCGAATTACAAACC : 120

\* 140 \* 160 \* 180  
TrMDHk : AAAAAAAATGGCGACTTGGTCAAAACACAACCTCCTCCACACAAGACCTTTCAGTTCCGG : 180

\* 200 \* 220 \* 240  
TrMDHk : TCTTCCTCGTCGACAAGACCAACTTCCCTAAGATGTTCCGCCACCCCATCCACCAA : 240

\* 260 \* 280 \* 300  
TrMDHk : AAATCCTACAAAATCACTCTTCTTCCGGGTGATGGCATAGGCCTGAAGTCGTTCCGTC : 300

\* 320 \* 340 \* 360  
TrMDHk : GCTAAAGACGTTCTTCTCCTCACTGGATCCATGGGATTAAACTTGAGTTCAAGAG : 360

\* 380 \* 400 \* 420  
TrMDHk : AAGCTTTGGGTGGTGCTGCTCTGATGCTACTGGAGTTCTTACCTGATGATACTCTT : 420

\* 440 \* 460 \* 480  
TrMDHk : TCTGTTGCTAACGAAATCTGATGCTGTTCTTGGTGCTATTGGAGGGTATAATGGGAT : 480

\* 500 \* 520 \* 540  
TrMDHk : AAAAAATGAGAACAGCTGAAGCCAGAAACTGGATTGCTTCAGCTACGAGAAGGGCTCAA : 540

\*  
TrMDHk : GTTTTGCTAACATCTCAGA : 558

Figure 85 Deducing amino acid sequence of TrMDH<sub>k</sub>

\* 20 \* 40 \* 60  
TrMDH<sub>k</sub> : MATCLQTQLLHTRPFQFRSSSSTRPTSLRCSAATPSTKKSYKITLLPGDGIGPEVVSVAK : 60

\* 80 \* 100 \* 120  
TrMDH<sub>k</sub> : DVLLLTIHGIKLEFQEKLGGAAALDATGVPLPDDTLSVAKQSDAVLLGAIGGYKWDKN : 120

\* 140  
TrMDH<sub>k</sub> : EKQLKPETGLLQLREGLQVFANLR : 144

Figure 86 Consensus contig nucleotide sequence of TrPEPCa

\* 20 \* 40 \* 60  
TrPEPCa : GNNACATTNCCGAATGCTGCTGAACTAGGGAGTGATTCCCTGGAGCCTATGTCATCTCT : 60

\* 80 \* 100 \* 120  
TrPEPCa : ATGGCCTCAAGTGCAAGCGATGTCCTTGCAGTAGAGCTTTACAGAAGGATGCACGTCTT : 120

\* 140 \* 160 \* 180  
TrPEPCa : ACAGTTGTGGAGAATTAGGAAGAGCATGTCGGGTGGAACGCTTCGGGTGGTTCCCTCTA : 180

\* 200 \* 220 \* 240  
TrPEPCa : TTTGAAACTGTGCAAGACCTGAGAGGAGCTGGTGCAGTTATCAGAAAACCTTTATCAATC : 240

\* 260 \* 280 \* 300  
TrPEPCa : GATTGGTACCGCCAACACATCATTAAGAACCATAACGGACACCAAGAGGTTATGGTCGGT : 300

\* 320 \* 340 \* 360  
TrPEPCa : TATTCTGATTCTGGTAAAGATGCCGGCGCTTACTGCTGCTTGGAACTTTACAAAGCT : 360

\* 380 \* 400 \* 420  
TrPEPCa : CAAGAGGATGTAGTGGCTGCTTGCATAAGTACGATACTAAGGTTACTTGTCCACGGC : 420

\* 440 \* 460 \* 480  
TrPEPCa : CGCGGAGGGAGTATTGGACGTGGCGGGAGGCCAACATATCTGGCTATTCAAGTCCCAGCCA : 480

\* 500 \* 520 \* 540  
TrPEPCa : CCTGGCTCTGTGATGGAACCCCTCGGTCAACTGAGCAGGGAGAGATGGTGCAGGCCGAG : 540

\* 560 \* 580 \* 600  
TrPEPCa : TTTGGGTTGCCACAGACAGCAGTTAGACAACCTGAAATATACACAACAGCTGTGCTACTT : 600.

\* 620 \* 640 \* 660  
TrPEPCa : GCTACACGTGTCGCCACCACCTCCCACCTCGAGAAGAAAAATGGCGTAATCTAATGGAAGAC : 660

\* 680 \* 700 \*  
TrPEPCa : ATNTCAAAAATCAGTTGTCAGTCCTACCGCAGTGTAGTCTATGAAAATCCAGN : 713

Figure 87 Deduced amino acid sequence of TrPEPCA

\* 20 \* 40 \* 60  
TrPEPCA : XTXPNAELGSDSLGAYVISMASSASDV LAVELLQKDARLTVC GELGRACPGGTLRVVPL : 60

\* 80 \* 100 \* 120  
TrPEPCA : FETVQDLRGAGAVIRKLLSIDWYRQHIIKNHNHGQEVMVGYS DSGKDAGRFTA AWE LYKA : 120

\* 140 \* 160 \* 180  
TrPEPCA : QEDVVAACNKYDTKVTLFHGRGGSIGRGGGPTYLAIQSOPPGSVMGTLRSTEQGEMVQAE : 180

\* 200 \* 220 \*  
TrPEPCA : FGLPQTAVRQLEIYT TAVLLATRRPPLPPREEKWRNLMEDXSKISCQS YRSVVYENP : 237

Figure 88 Nucleotide sequences of nucleic acid fragments contributing to the consensus contig sequence TrPEPCa

	*	20	*	40	*	60	
TrPEPCa1	:	GNNACATTNCCGAATGCTGCTGAACTAGGGAGTGATTCCCTTGGAGCCTATGTCATCTCT					: 60
TrPEPCa2	:	- - - - -					: -
TrPEPCa3	:	- - - - -					: -
	*	80	*	100	*	120	
TrPEPCa1	:	ATGGCCTCAAGTGCAGCGATGTCCTTGCAGTAGAGCTTTT-CAGAAGGGATGCACGACTT					: 119
TrPEPCa2	:	- - - - -	GNACTTTACAGAAGGGATGCACGTCTT				: 27
TrPEPCa3	:	- - - - -	AGCTTTACAGAAGGGATGCACGTCTT				: 26
	*	140	*	160	*	180	
TrPEPCa1	:	GCTGGCTATTGGAGAGTTGGAAAGAGCATGTCCTGGTGGAACGCTGGGTGGTGCCTCTA					: 179
TrPEPCa2	:	ACAGTTTGTGGAGAATTAGGAAGAGCATGTCGGGTGGAACGCTTCGGGTGGTCTCTA					: 87
TrPEPCa3	:	ACAGTTTGTGGAGAATTAGGAAGAGCATGTCGGGTGGAACGCTTCGGGTGGTCTCTA					: 86
	*	200	*	220	*	240	
TrPEPCa1	:	TTTGAAGACTGTGAGGACCTAGAGGAGCTGGTGCAGTTATCAGAAAACCTTTATCGATA					: 239
TrPEPCa2	:	TTTGAAGACTGTGCAAGACCTGAGAGGAGCTGGTGCAGTTATCAGAAAACCTTTATCAATC					: 147
TrPEPCa3	:	TTTGAAGACTGTGCAAGACCTGAGAGGAGCTGGTGCAGTTATCAGAAAACCTTTATCAATC					: 146
	*	260	*	280	*	300	
TrPEPCa1	:	GAGTGGTACCGGAAACACATCATTAAGAACCAAAAGGACATCAAGAGGTTATGGTGGAA					: 299
TrPEPCa2	:	GATTGGTACCGCCAACACATCATTAAGAACCATAACGGACACCAAGAGGTTATGGTCGGT					: 207
TrPEPCa3	:	GATTGGTACCGCCAACACATCATTAAGAACCATAACGGACACCAAGAGGTTATGGTCGGT					: 206
	*	320	*	340	*	360	
TrPEPCa1	:	TATTCTGATTCTGGTAAAGATGCCGGCGCTTACTGCTGCTGGAACTTTACAAAGCT					: 359
TrPEPCa2	:	TATTCTGATTCTGGTAAAGATGCCGGCGCTTACTGCTGCTGGAACTTTACAAAGCT					: 267
TrPEPCa3	:	TATTCTGATTCTGGTAAAGATGCCGGCGCTTACTGCTGCTGGAACTTTACAAAGCT					: 266
	*	380	*	400	*	420	
TrPEPCa1	:	CAGGAGGATGTGTAGCTGCTTGCATGATTAAGCTATAAAGTTAACAGTGTTCAGGGC					: 419
TrPEPCa2	:	CAAGAGGATGTAGTGGCTGCTTGCATAAGTACGATACTAAGGTTACTTGTCCACGGC					: 327
TrPEPCa3	:	CAAGAGGATGTAGTGGCTGCTTGCATAAGTACGATACTAAGGTTACTTGTCCACGGC					: 326
	*	440	*	460	*	480	
TrPEPCa1	:	CGGGGAGGCGAGTATTGGCGAGGGGGGGCCCTACATATCTGGCTATTCACTCCCACCA					: 479
TrPEPCa2	:	CGCGGGAGGGAGTATTGGACGTGGCGGAGGCCAACATATCTGGCTATTCACTCCCAGGCC					: 387
TrPEPCa3	:	CGCGGGAGGGAGTATTGGACGTGGCGGAGGCCAACATATCTGGCTATTCACTCCCAGGCC					: 386
	*	500	*	520	*	540	
TrPEPCa1	:	CCTGGCTCTGTGATGGGAACACTTCGGCTACTGAGCAGGGAGAATGGTAGAGGCCAG					: 539
TrPEPCa2	:	CCTGGCTCTGTGATGGGAACCCCTTCGGTCAACTGAGCAGGGAGAGATGGTGAGGCCAG					: 447
TrPEPCa3	:	CCTGGCTCTGTGATGGGAACCCCTTCGGTCAACTGAGCAGGGAGAGATGGTGAGGCCAG					: 446
	*	560	*	580	*	600	
TrPEPCa1	:	TTTGGGTTACACAGAAGCAGTGTAGACAACCTGANN-----					: 576
TrPEPCa2	:	TTTGGGTTGCCACAGACAGCAGTGTAGACAACCTGAAATATACACAAACAGCTGTGCTACTT					: 507
TrPEPCa3	:	TTTGGGTTGCCACAGACAGCAGTGTAGACAACCTGAAATATACACAAACAGCTGTGCTACTT					: 506

\* 620 \* 640 \* 660

TrPEPCa1 : -----  
TrPEPCa2 : GCTACACGTCGCCACCACTCCCACCTCGAGAAGAAAAATGGCGTAATCTAATGGAAGAC : 567  
TrPEPCa3 : GCTACACGTCGCCACCACTCCCACCTCGAGAAGAAAAATGGCGTAATCTAATGGAAGAC : 566

\* 680 \* 700 \*

TrPEPCa1 : -----  
TrPEPCa2 : ATN----- : 570  
TrPEPCa3 : ATTCACAAAATCAGTTGTCAGTCCTACCGCAGTGTAGTCATGAAAATCCAGN : 619

Se 89. Consensus contig nucleotide sequence of TrPEPCb

\* 20 \* 40 \* 60  
TrPEPCb : GNAAGGGACAAGCTCTATCGTACTCGTGAGCGGTCTCGCTATCTTAGCTCATGGCTAT : 60

\* 80 \* 100 \* 120  
TrPEPCb : TCTGAAATTCCCTGAAGAAGGCCACATTCACCGATGTTGATGAGTTCTTGGAACCTCTTGAA : 120

\* 140 \* 160 \* 180  
TrPEPCb : CTATGCTACAGATCACTCTGTGCTTGGTGATCGTGCATTGCCATGGAACCCCTCTT : 180

\* 200 \* 220 \* 240  
TrPEPCb : GATTTCCTTGAGGCAAGTTCCACTTTGGACTGTCACTGGTAAGACTTGATATAAGGCAA : 240

\* 260 \* 280 \* 300  
TrPEPCb : GAGTCAGATCGTCACACGGACGTGATGGATGCCATTACAAACATTGGAAATTGGATCC : 300

\* 320 \* 340 \* 360  
TrPEPCb : TACCAAGACTGGTCTGAAGAAAAAGACAGGAATGGCTTTGTCTGAGTTGGTGGCAA : 360

\* 380 \* 400 \* 420  
TrPEPCb : AGGCCGCTTTGGACCTGACCTACCTCAAACCGATGAAATTAGAGAAGTTTAGAGACA : 420

\* 440 \* 460 \* 480  
TrPEPCb : TTTCATGTCATAGCAGAACTTCCATCAGACAACTTGGAGCCTATATCATTGATGGCA : 480

\* 500 \* 520 \* 540  
TrPEPCb : ACTGCCCGTCTGATGTGCTAGCGGTTGAACCTCTTCAACGTGAATGCAAAATCAAGAAT : 540

\* 560 \* 580 \*  
TrPEPCb : CCGTTAAGAGTTGTTCCGTTGAGAAACTTGCTGATCTCGAGTCTGCTCCTGCTG : 598

Se 90 Deduced amino acid sequence of TrPEPCb

\* 20 \* 40 \* 60  
TrPEPCb : XRDKLYRTRERSRYLLAHGYSEIPEEATFTDVDEFLEPLELCYRSLCACGDRAIADGSLL : 60

\* 80 \* 100 \* 120  
TrPEPCb : DFLRQVSTFGLSLVRLDIIRQESDRHTDVMDAITKHLEIGSYQDWSEEKRQEWLSELVGK : 120

\* 140 \* 160 \* 180  
TrPEPCb : RPLFGPDLPQTDEIREVLETFHVIAELPSDNFGAYIISMATAPSDVLAVELLQRECKIKN : 180

\*  
TrPEPCb : PLRVVPLFEKLADLESAPA : 199

Table 91 Nucleotide sequences of nucleic acid fragments contributing to the consensus contig sequence TrPEPCb

	*            20            *            40            *            60	
TrPEPCb1 :	GNAAGGGACAAGCTCTATCGTACTCGTGAGCGGTCTCGCTATCTCTTAGCTCATGGCTAT	: 60
TrPEPCb2 :	GAAAGGGACAAGCTCTATCGTACTCGTGAGCGGTCTCGCTATCTCTTAGCTCATGGCTAT	: 60
	*            80            *            100            *            120	
TrPEPCb1 :	TCTGAAATTCCCTGAAGAACGCCACATTACCGATGTTGATGAGTTCTTGGAACCTCTTGAA	: 120
TrPEPCb2 :	TCTGAAATTCCCTGAAGAACGCCACATTACCGATGTTGATGAGTTCTTGGAACCTCTTGAA	: 120
	*            140            *            160            *            180	
TrPEPCb1 :	CTATGCTACAGATCACTCTGTGCTTGTGGTATCGTGCCTATTGCCATGGAACGCCTTCTT	: 180
TrPEPCb2 :	CTATGCTACAGATCACTCTGTGCTTGTGGTATCGTGCCTATTGCCATGGAACGCCTTCTT	: 180
	*            200            *            220            *            240	
TrPEPCb1 :	GATTCTTGAGGCAAGTTCCACTTTGGACTGTCACTGGTAAGACTTGATATAAGGCAA	: 240
TrPEPCb2 :	GATTCTTGAGGCAAGTTCCACTTTGGACTGTCACTGGTAAGACTTGATATAAGGCAA	: 240
	*            260            *            280            *            300	
TrPEPCb1 :	GAGTCAGATCGTCACACGGACGTGATGGATGCCATTACCAAACATTGGAAATTGGATCC	: 300
TrPEPCb2 :	GAGTCAGATCGTCACACGGACGTGATGGATGCCATTACCAAACATTGGAAATTGGATCC	: 300
	*            320            *            340            *            360	
TrPEPCb1 :	TACCAAGACTGGTCTGAAGAAAAAGACAGGAATGGCTTGTCTGAGTTGGTTGGCAAA	: 360
TrPEPCb2 :	TACCAAGACTGGTCTGAAGAAAAAGACAGGAATGGCTTGTCTGAGTTGGTTGGCAAA	: 360
	*            380            *            400            *            420	
TrPEPCb1 :	AGGCCGCTTTGGACCTGACCTACCTCAAACCGATGAAATTAGAGAAGTTTAGAGACA	: 420
TrPEPCb2 :	AGGCCGCTTTGGACCTGACCTACCTCAAACCGATGAAATTAGAGAAGTTTAGAGACA	: 420
	*            440            *            460            *            480	
TrPEPCb1 :	TTTCATGTCAAGCAGAACTTCCATCAGACAACCTGGAGCCTATATCATTGATGGCA	: 480
TrPEPCb2 :	TTTCATGTCAAGCAGAACTTCCATCAGACAACCTGGAGCCTATATCATTGATGGCA	: 480
	*            500            *            520            *            540	
TrPEPCb1 :	ACTGCCCGTCTGATGTGCTAGCGGTTGAACCTCTTCAACGTGAATGCAAAATCAAGAAT	: 540
TrPEPCb2 :	ACTGCCCGTCTGATGTGCTAGCGGTTGAACCTCTTCAACGTGAATGCAAAATCAAGAAT	: 540
	*            560            *            580            *	
TrPEPCb1 :	CCGTTAAGAGTTGTTCCGTTGTTGAGAAACTTGCTGATCTCGAGTCGCTCCTGCTG	: 598
TrPEPCb2 :	CCGTTAAGAGTTGTTCCGTTGTTGAGAAACTTGCTGATCTCGN-----	: 584

e 92 Consensus contig nucleotide sequence of TrPEPCC

\* 20 \* 40 \* 60  
TrPEPCC : GTCACATGACAAACNATATCTCCCTTCTAACTCCGTGATCAAGGCAGTTAGTTAGTTA : 60

\* 80 \* 100 \* 120  
TrPEPCC : CACAAATTGCTGTTAGGTTCGTTGACTTCCCCTGCAATCCATAGTATCTTGGAGGAA : 120

\* 140 \* 160 \* 180  
TrPEPCC : CAAACTAGATTTCCACCTAGGTCGTACAGAGATTTCCCTTCACATTTFTCTTTTC : 180

\* 200 \* 220 \* 240  
TrPEPCC : ATATAATAACTCAACACTTTCTAGCTACTTAGTACTGTGTAACACAAATTTATT : 240

\* 260 \* 280 \* 300  
TrPEPCC : CATTATGGCTACTCCTCGAACATTGAAAAAATGGCTTCAATTGATGCTCAATTGAGACT : 300

\* 320 \* 340 \* 360  
TrPEPCC : ACTAGCACCAAGGAAAGTTCTGATGATGATAAACCTGTCGAGTATGATGCTTGTATT : 360

\* 380 \* 400 \* 420  
TrPEPCC : GGATCGATTCTTGACATTCTCAAGATTTGCATGGAGAAGATATCAGACAAACTGTTCA : 420

\* 440 \* 460 \* 480  
TrPEPCC : AGATTGTTATGAGTTATCGGCAGAGTATGAAGGGGAGCTTAAGCCGGAGAAATTGGAGGA : 480

\* 500 \* 520 \* 540  
TrPEPCC : ACTTGGGAATATGCTTACTGGTCTTGATGCTGGAGATTCTATTGTTATAGCAAATCATT : 540

\* 560  
TrPEPCC : TTCTCATATGCTTAATTGGCAAACCTGGCAGAGN : 575

Se 93 Deduced amino acid sequence of TrPEPCC

\* 20 \* 40 \* 60  
TrPEPCC : MATPRNIEKMASIDAQLRLLAPRKVSDDDKLVEYDALLLDRFLDILQDLHGEDIRQTVQD : 60

\* 80 \* 100 \*  
TrPEPCC : CYELSAEYEGERKPEKLEELGNMLTGGLAGDSIVIAKSFSHMLNLNLAE : 110

Table 94 Nucleotide sequences of nucleic acid fragments contributing to the consensus contig sequence TrPEPcC

	*	20	*	40	*	60		
TrPEPcC1	:	GTCACATGAC	NAC	ATATCTCCCTTCTCTA	ACTCCGTGATCAAGGC	GTTAGTTAGTTA	: 60	
TrPEPcC2	:	-----TGACAAACN	A	ATATCTCCCTTCTCTA	ACTCCGTGATCAAGGC	GTTAGTTA	: 54	
	*	80	*	100	*	120		
TrPEPcC1	:	CACAAATTGCTGTTAGGTT	TGACTTTCCC	GTCATCCATAGTATCTGGAGGAA			: 120	
TrPEPcC2	:	CACAAATTGCTGTTAGGTT	TGACTTTCCC	GTCATCCATAGTATCTGGAGGAA			: 114	
	*	140	*	160	*	180		
TrPEPcC1	:	CAAAC	ACTAGATT	TTCCACCTAGGT	CGTCACGAGAT	TTTCTTC	ACTATT	: 180
TrPEPcC2	:	CAAAC	ACTAGATT	TTCCACCTAGGT	CGTCACGAGAT	TTTCTTC	ACTATT	: 174
	*	200	*	220	*	240		
TrPEPcC1	:	ATATAATAACT	CAACACT	TTTCTAGCTACT	AGTACTGTGTAACACA	AAATT	TTATT	: 240
TrPEPcC2	:	ATATAATAA	CTCAACACT	TTTCTAGCTACT	AGTACTGTGTAACACA	AAATT	TTATT	: 234
	*	260	*	280	*	300		
TrPEPcC1	:	CATTATGGCTACT	CCCGAACATTG	AAAAAATGGCTTC	ATTGATGCTCAATTGAGACT			: 300
TrPEPcC2	:	CATTATGGCTACT	CCCGAACATTG	AAAAAATGGCTTC	ATTGATGCTCAATTGAGACT			: 294
	*	320	*	340	*	360		
TrPEPcC1	:	ACTAGCACCAAGGAA	AGTTCTGATGATGATAA	ACTTGTCGAGTATGATG	C	TTGTTATT		: 360
TrPEPcC2	:	ACTAGCACCAAGGAA	AGTTCTGATGATGATAA	ACTTGTCGAGTATGATG	C	TTGTTATT		: 354
	*	380	*	400	*	420		
TrPEPcC1	:	GGATCGATT	CCCTGACATT	CTCAAGATTG	CATGGAGAAGATATC	AGACAA	ACTGTTCA	: 420
TrPEPcC2	:	GGATCGATT	CCCTGACATT	CTCAAGATTG	CATGGAGAAGATATC	AGACAA	ACTGTTCA	: 414
	*	440	*	460	*	480		
TrPEPcC1	:	AGATTGTTATGAGTT	ATCGGCAGAGTATGAAGGGGAGCTT	A	GGCCGGAGAAATTGGAGGA			: 480
TrPEPcC2	:	AGATTGTTATGAGTT	ATCGGCAGAGTATGAAGGGGAGCTT	A	GGCCGGAGAAATTGGAGGA			: 474
	*	500	*	520	*	540		
TrPEPcC1	:	ACTTGGGAATATGCTT	ACTGGTCTTGATGCTGGAGATT	CTATTGTT	ATAGCAAA	ATCATT		: 540
TrPEPcC2	:	ACTTGGGAATATGCTT	ACTGGTCTTGATGCTGGAGATT	CTATTGTT	ATAGCAAA	ATCATT		: 534
	*	560	*					
TrPEPcC1	:	TTCTCATATGCTTAA	TTGGCAA	ACTTGGCAGAGN				: 575
TrPEPcC2	:	TTN-----						: 537

Figure 95 Nucleotide sequence of TrPEPCd

\* 20 \* 40 \* 60  
TrPEPCd : AGAAGATCTCATGTTGAGTTGTCTATGTGGCGCTGCAACGACGAGCTCCGTGTTAGAGC : 60

\* 80 \* 100 \* 120  
TrPEPCd : TGAAGAGCTTCATAGATCCTCAAAGAAAGATGCAAAACATTATATTGAGTTTGGAAACA : 120

\* 140 \* 160 \* 180  
TrPEPCd : GATTCCCTCAAACGAGCCATATCGTGTATTCTGGAGGTGTGAGGGACAAACTGTATAA : 180

\* 200 \* 220 \* 240  
TrPEPCd : TACACGTGAACGTGCTCGACAGTTATTAGCAAATGGAACCTCTGACATCCTTGAAAGAGAC : 240

\* 260 \* 280 \* 300  
TrPEPCd : AACCTTCACGAATGTTGAGCAGTTCTGGAGCCTCTGAACTGTGTATAGGTCACTTTG : 300

\* 320 \* 340 \* 360  
TrPEPCd : TGCAATGGTGACCGATCAATAGCAGACGGAAAGCCTCTGATTTCTTGCAGACAAGTTTC : 360

\* 380 \* 400 \* 420  
TrPEPCd : TACATTTGGACTTCACTTGTAAAGACTCGACATCCGTCAAGAGTCAGACAGGCCACACAGA : 420

\* 440 \* 460 \* 480  
TrPEPCd : CGTTATGGATGCAATTACAAAACACTTGGAGATTGGATCTTACCGAGAATGGTCGGAAGA : 480

\* 500 \* 520 \* 540  
TrPEPCd : ACGCAGGCAGGAATGGCTTGTCTGAGCTTAGTGGAAAACGCCCTCTTCGGCCATGA : 540

\* 560 \* 580 \* 600  
TrPEPCd : TCTTCCTAACAGACAGAAGAAATTGCCGATGTTAGATACCTNCACGTNATTCANAAC : 600

\* 620 \* 640 \* 660  
TrPEPCd : TNCCCTCANATAGCTTGGTGCCTATATCATCTCAATGGCAACCTCCCCATCTGATGTGCT : 660

\* 680 \* 700 \* 720  
TrPEPCd : AGCTGTCGAGCTTTACAACGTGAATGTCATGTGAAGCAGCCGTTAANAGTTGTTCCACT : 720

\* 740 \* 760 \* 780  
TrPEPCd : GTTGAAAAGCTGCCNGTCTTGAGTCTGCTCCTGCTGCCAGCGCTTTTTNTTNTAGA : 780

\* 800 \* 820 \* 840  
TrPEPCd : TTGGGNCANAACGNNNTAATGGAAAGCAGAAGTTNTGATAGGTACTCANACTNGGGAAA : 840

\*  
TrPEPCd : AGATGCTGGCCGNN : 854

e 96 Deduced amino acid sequence of TrPEPCd

\* 20 \* 40 \* 60  
TrPEPCd : EDLMFELSMWRCNDELRVRAEELHRSSKKDAKHYIEFWKQIPPNEPYRVLGGVRDKLYN : 60

\* 80 \* 100 \* 120  
TrPEPCd : TRERARQLLANGTSDILEETTFTNVEQFLEPLELCYRSLCACGDRSIADGSLLDFLRQVS : 120

\* 140 \* 160 \* 180  
TrPEPCd : TFGLSLVRLDIQRQESDRHTDVMDAITKHLEIGSYREWSEERRQEWLSELSGKRPLFGHD : 180

\* 200 \* 220 \* 240  
TrPEPCd : LPKTEEIADVLDTXHXISXLXSXSFAYIISMATSPSDVLAVELLQRECHVKQPLXVVPL : 240

\* 260 \* 280  
TrPEPCd : FEKLAXLESAPAAKARFXLDWXXTXXMESRSXDRYSXXGKDAGX : 283

## 97 Nucleotide sequence of TrPEPc

\* 20 \* 40 \* 60  
 TrPEPc<sub>e</sub> : GTTCACTGTCTCTGNCCAATTTCCTCCCTGTCTCTTTCTTCTTCCTCGTA : 60

 \* 80 \* 100 \* 120  
 TrPEPc<sub>e</sub> : TCTTACTGCCTCATTACACGGGTGAGAAGGAGTGAATTGCTCCAATGGCAACAAACAAAA : 120

 \* 140 \* 160 \* 180  
 TrPEPc<sub>e</sub> : TGGAAAAAATGGCATCAATTGATGCACAGCTTAGACAATTAGTACCAAGCAAAGTTAGTG : 180

 \* 200 \* 220 \* 240  
 TrPEPc<sub>e</sub> : AAGATGATAAACCTATTGAGTATGATGCTTGTGATCGGTTCTGATATCCTTC : 240

 \* 260 \* 280 \* 300  
 TrPEPc<sub>e</sub> : AGGATTTACATGGAGAGGATCTGAAAGATTCTGTTCAAGAAGTGTATGAACCTTCTGCCG : 300

 \* 320 \* 340 \* 360  
 TrPEPc<sub>e</sub> : AGTATGAAAGAAAGCATGATCCTAAGAAACTTGAAGAGAGCTCGGAAATTGATAACAAGTT : 360

 \* 380 \* 400 \* 420  
 TrPEPc<sub>e</sub> : TAGATGCAGGAGATTCAATTGTTGCTAAGTCCTTCGACATGCTTAACCTGGCCA : 420

 \* 440 \* 460 \* 480  
 TrPEPc<sub>e</sub> : ACTTAGCTGAAGAGGTTTCAGATTGCTCATCGTCGAAGGAACAAAGTTGAAGAAAGGAGATT : 480

 \* 500 \* 520 \* 540  
 TrPEPc<sub>e</sub> : TTAGGGATGAGAGCAATGCAACTACCGAATCAGACATCGAAGAAACTCTTAAGAGACTTG : 540

 \* 560 \* 580 \* 600  
 TrPEPc<sub>e</sub> : TGTTTAATATGAAGAAATCTCCTCAGGAAGTTNTGATGCGTTGAAGAACNNACCGTTG : 600

 \* 620 \* 640 \* 660  
 TrPEPc<sub>e</sub> : ATTTGGTTCTTACTGCTCATCCCACTCAGTCCGTTGANGNCCNCTGCTTCCNNNGCCT : 660

 \* 680 \*  
 TrPEPc<sub>e</sub> : GGNACGGGNACCGCNCTGNCTATCNNACTGNNN : 693

re 98 Deduced amino acid sequence of TrPEPCe

\* 20 \* 40 \* 60  
TrPEPCe : MATNKMEKMASIDAQLRQLVPAKVSEDDKLIEYDALLLDRFLDILQDLHGEDLKDSVQEV : 60

\* 80 \* 100 \* 120  
TrPEPCe : YELSAEYERKHDPKKLEELGNLITSLDAGDSIVVAKSFSHMLNLANLAEVQIAHRRRNK : 120

\* 140 \* 160 \* 180  
TrPEPCe : LKKGDFRDESNATTESDIEETLKRLVFNMKKSPQEVDALKNXTVDLVTAHPTQSVRXX : 180

\*  
TrPEPCe : LLPXAWXGXRXYYXTX : 196

Se 99 Consensus contig nucleotide sequence of TrCSa

\* 20 \* 40 \* 60  
TrCSa : GNNNCNCNACCATTACATTAATNACACTTCCNCTTCGCCTGTTCTTCTCTCAA : 60

\* 80 \* 100 \* 120  
TrCSa : TATAAAGACCAATTCAATTCCAATTCTTTGGATCCGAAATCATTCACTACCGGTCT : 120

\* 140 \* 160 \* 180  
TrCSa : TCTCTCTCTCGCGTTCAAACCCTAGTTGTTGATTGATCTAAATGGCGTTCTT : 180

\* 200 \* 220 \* 240  
TrCSa : TCGAAGCGTTCTGCCTTCAAAACTACGATCTCGTGTGGGTCAACAACCTAGTCTTGC : 240

\* 260 \* 280 \* 300  
TrCSa : TAATTCAAGTTAGATGGCTCCAAACTCCAAGCTCCAGTAACACTGATCTTATTCTGAGAT : 300

\* 320 \* 340 \* 360  
TrCSa : GAAGGAGCTAGTTCCAGAGTATCAGGAACGTGTTAAGAAGTTGAAGAAAGACCATGGAAG : 360

\* 380 \* 400 \* 420  
TrCSa : TGTTGAATTGGGAAAAATCACAGCTGATATGGTACTTGGTGAATGAGAGGAATGACTGC : 420

\* 440 \* 460 \* 480  
TrCSa : TTTAGTGTGGCTAGGCTCAGCTGTTGACCCAGATGAGGGATTGCTTAGGGCATGAC : 480

\* 500 \* 520 \* 540  
TrCSa : AATTCCCTGACTGCCAGAAAACACTCCAGGTGCTTCTGGTGGGGAGCCTTGCCCCGA : 540

\* 560 \* 580 \* 600  
TrCSa : GGCTATACTGTGGCTTCTATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCAATT : 600

\* 620 \* 640 \* 660  
TrCSa : AGCTCACGAATTGCGAAGTCGTGAAAAATCCCAGAGTATGCTTACAAGGCAATTGATGC : 660

\* 680 \* 700 \* 720  
TrCSa : ACTGCCTTTCTGCTCATCCAATGACACAATTAGTACTGGTGTAAATGCCCTCCAGGT : 720

\* 740 \* 760 \* 780  
TrCSa : GGAGAGTGAGTTACAAAGGCATACGAGAGTGGGATACATAAGTCAAGGTATTGGGAGCC : 780

\* 800 \* 820 \* 840  
TrCSa : AACTTATGAGGATAGCTTGAATTAAATTGCTCGTTGCCTGGAATTGCTGCCTATATTAA : 840

\* 860 \* 880 \* 900  
TrCSa : TCGACGGATATAAGGATGGAAAAATCATACCATTGGATGATTCTTGGATTATGGTGC : 900

\* 920 \* 940 \* 960  
TrCSa : AAACTATGCTCACATGTTAGGATTTGATGATCCAGAACGCTGGAGTTATGAGGCTGTA : 960

\* 980 \* 1000 \* 1020  
TrCSa : TATTTCTATCCATAGT GATCATGAAGGNGGCAAC GTTAGTTCTCACACAGCTCACCTAGT : 1020

\* 1040 \* 1060 \* 1080  
TrCSa : TGCTAGTTCACTATCAGATCCTTATCTTG CATT CGCAGCTGCTCTGAATGGTTAGCTGG : 1080

\* 1100 \* 1120 \* 1140  
TrCSa : CCCACTGCATGGTTAGCCAATCAGGAAGTTCTACGATGGATCAGAACATAGTTAAGGA : 1140

\* 1160 \* 1180 \* 1200  
TrCSa : GTTTGGAACTCCAAACATAAGTACAGAACAAATTGAGCGACTACATT CATAAAACATTGAA : 1200

\* 1220 \* 1240 \* 1260  
TrCSa : CAGTGGCCAGGTTG CCTGGATATGGACATGGAGTTTGC GCAATACAGACCCAAGATA : 1260

\* 1280 \* 1300  
TrCSa : CACTTGCCAGAGGGAGTTGCATTGAAGCATTGCCTAATGATCCAN : 1307

Se 100 Deduced amino acid sequence of TrCSa

\* 20 \* 40 \* 60  
TrCSa : MAFFRSVSALSKLRSRVGQQPSLANSVRWLQTPSSNTDLYSEMKELVPEYQERVKKLKK : 60

\* 80 \* 100 \* 120  
TrCSa : DHGSVELGKITADMVLGGMRGMTELVWLGSAVDPDEGIRFRGMTIPDCQKTLPGAFPGGE : 120

\* 140 \* 160 \* 180  
TrCSa : PLPEAILWLLTGKVPSKEQVDSLAEHLRSRAKIPEYAYKAIDALPVSAHPMTQFSTGVM : 180

\* 200 \* 220 \* 240  
TrCSa : ALQVESEFTKAYESGIHKSRYWEPTYEDSLNLIARLPGIAAYIYRRIYKDGTIIPLDDSL : 240

\* 260 \* 280 \* 300  
TrCSa : DYGANAHMLGFDDPETLEFMRLYISIHSDHEGNVSSHTAHLVASSLSDPYLAFAAALNG : 300

\* 320 \* 340 \* 360  
TrCSa : LAGPLHGLANQEVLRWIRNIVKEFGTPNISTEQLSDYIHKTLNNSGQVVPGYGHGVLRNTD : 360

\*  
TrCSa : PRYTCQREFALKHLPNDP : 378



	* 380	* 400	* 420	
TrCSa1 :	TGTTGAATTGGGAAAAATCACAGCTGATATGGTACTTGGTGGAAATGAGAGGAATGACTGC		: 420	
TrCSa2 :	TGTTGAATTGGGAAAAATCACAGCTGATATGGTACTTGGTGGAAATGAGAGGAATGACTGC		: 404	
TrCSa3 :	TGTTGAATTGGGAAAAGTCACAGCTGATATGGTACTTGGTGGAAATGAGAGGAATGACAGC		: 340	
TrCSa4 :	TGTTGAATTGGGAAAAATCACAGCTGATATGGTACTTGGTGGAAATGAGAGGAATGACTGC		: 307	
TrCSa5 :	- - - - - GNGGAAAAATACAGCTGATATGGTACTTGGTGGAAATGAGAGGAATGACTGC		: 51	
TrCSa6 :	- - - - -		: 16	
TrCSa7 :	- - - - -		:	
	* 440	* 460	* 480	
TrCSa1 :	TTTAGTGTGGCTAGGCTCAGCTGTTGACCCAGATGAGGGAAATCGCTT TAGGGGCATGAC		: 480	
TrCSa2 :	TTTAGTGTGGCTAGGCTCAGCTGTTGACCCAGATGAGGGAAATCGCTT TAGGGGCATGAC		: 464	
TrCSa3 :	TTTAGTGTGGCTAGGCTCAGCTGTTGACCCAGATGAGGGAAATCGCTT TAGGGGCATGAC		: 400	
TrCSa4 :	TTTAGTGTGGCTAGGCTCAGCTGTTGACCCAGATGAGGGAAATCGCTT TAGGGGCATGAC		: 367	
TrCSa5 :	TTTAGTGTGGCTAGGCTCAGCTGTTGACCCAGATGAGGGAAATCGCTT TAGGGGCATGAC		: 111	
TrCSa6 :	TTTAGTGTGGCTAGGCTCAGCTGTTGACCCAGATGAGGGAAATCGCTT TAGGGGCATGAC		: 74	
TrCSa7 :	- - - - -		:	
	* 500	* 520	* 540	
TrCSa1 :	AATTCTGACTGCCAGAAAACACTTCCAGGTGCTT CTCAGGTGGGAGCCTTGCCCCGA		: 540	
TrCSa2 :	AATTCTGACTGCCAGAAAACACTTCCAGGTGCTT CTCAGGTGGGAGCCTTGCCCCGA		: 524	
TrCSa3 :	AATTCTGACTGCCAGAAAACACTTCCAGGTGCTT CTCAGGTGGGAGCCTTGCCCCGA		: 460	
TrCSa4 :	AATTCTGACTGCCAGAAAACACTTCCAGGTGCTT CTCAGGTGGGAGCCTTGCCCCNA		: 427	
TrCSa5 :	AATTCTGACTGCCAGAAAACACTTCCAGGTGCTT CTCAGGTGGGAGCCTTGCCCCGA		: 171	
TrCSa6 :	AATTCTGACTGCCAGAAAACACTTCCAGGTGCTT CTCAGGTGGGAGCCTTGCCCCGA		: 133	
TrCSa7 :	- - - - -		:	
	* 560	* 580	* 600	
TrCSa1 :	GGCTATACTGTGGCTTCTATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCA		: 600	
TrCSa2 :	GGCTATACTGTGGCTTCTATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCA		: 584	
TrCSa3 :	GGCTATACTGTGGCTTCTATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCA		: 520	
TrCSa4 :	GGCTATACTGTGGCTTCTATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCA		: 456	
TrCSa5 :	GGCTATACTGTGGCTTCTATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCA		: 231	
TrCSa6 :	GGCTATACTGTGGCTTCTATTGACCGGAAAGGTACCAAGTAAAGAGCAAGTAGATTCA		: 193	
TrCSa7 :	- - - - -		:	
	* 620	* 640	* 660	
TrCSa1 :	AGCTCACGAATTGCGAAGTCGTGCAAAAATCCCAGAGTATGCTTACAAGGAATTGATGC		: 660	
TrCSa2 :	AGCN-----		: 588	
TrCSa3 :	AGCTCACGAATTGCGAAGTCGTGCAAAAATCCCAGAGTATGCTTACAAGGAATTGATGC		: 580	
TrCSa4 :	- - - - -		:	
TrCSa5 :	AGCTCACGAATTGCGAAGTCGTGCAAAAATCCCAGAGTATGCTTACAAGGAATTGATGC		: 291	
TrCSa6 :	AGCTCACGAATTGCGAAGTCGTGCAAAAATCCCAGAGTATGCTTACAAGGAATTGATGC		: 253	
TrCSa7 :	- - - - -		:	
	* 680	* 700	* 720	
TrCSa1 :	ACTGCCTGTTCTGCTCATCCAATGACACAA-----		: 692	
TrCSa2 :	- - - - -		:	
TrCSa3 :	ACTGCCTGTTCTGCTCATCCAATGACACAAATTAGTACTGGTGTAAATGCCCTCCAGGT		: 640	
TrCSa4 :	- - - - -		:	
TrCSa5 :	ACTGCCTGTTCTGCTCATCCAATGACACAAATTAGTACTGGTGTAAATGCCCTCCAGGT		: 351	
TrCSa6 :	ACTGCCTGTTCTGCTCATCCAATGACACAAATTAGTACTGGTGTAAATGCCCTCCAGGT		: 313	
TrCSa7 :	- - - - -		:	

\* 740 \* 760 \* 780

TrCSa1 : -  
TrCSa2 : -  
TrCSa3 : GGAGAGT GAGTTACAAAGGCATA[GGAGAGT GGGATACATN] : 681  
TrCSa4 : -  
TrCSa5 : GGAGAGT GAGTTACAAAGGCATA[CGAGAGT GGGATACATAAGTCAAGG]TATTGGGAGCC : 411  
TrCSa6 : GGAGAGT GAGTTACAAAGGCATA[CGAGAGT GGGATACATAAGTCAAGG]TATTGGGAGCC : 373  
TrCSa7 : -[CAGAGT GGGATACNT-AGT-AAGG]ATTGGGAGCC : 34

\* 800 \* 820 \* 840

TrCSa1 : -  
TrCSa2 : -  
TrCSa3 : -  
TrCSa4 : -  
TrCSa5 : AACTTATGAGGATAGCTGAATTAAATTGCTCGTTGCCTGGAATTGCTGCCTATATTAA : 471  
TrCSa6 : AACTTATGAGGATAGCTGAATTAAATTGCTCGTTGCCTGGAATTGCTGCCTATATTAA : 433  
TrCSa7 : -ACTTATGAGGAT[GCTTGAAATTAAATTGCTCGTTGCCTGGAATTGCTGCCTATATTAA] : 92

\* 860 \* 880 \* 900

TrCSa1 : -  
TrCSa2 : -  
TrCSa3 : -  
TrCSa4 : -  
TrCSa5 : TCGACGGATATA[CAAGGATGGAAAAATCATACCATTGGATGATTCTTGGATTATGGTGC] : 531  
TrCSa6 : TCGACGGATATA[CAAGGATGGAAAAATCATACCATTGGATGATTCTTGGATTATGGTGC] : 493  
TrCSa7 : TCGACGGATATA[CAAGGATGGAAAAATCATACCATTGGATGATTCTTGGATTATGGTGC] : 152

\* 920 \* 940 \* 960

TrCSa1 : -  
TrCSa2 : -  
TrCSa3 : -  
TrCSa4 : -  
TrCSa5 : AAAC[TATGCTCACATGTTAGGATTGATGATCCAGAAACGCTGGAGTT]ATGAGGCTGTA : 591  
TrCSa6 : AAAC[TATGCTCACATGTTAGGATTGATGATCCAGAAACGCTGGAGTT]ATGAGGCTGTA : 553  
TrCSa7 : AAAC[TATGCTCACATGTTAGGATTGATGATCCAGAAACGCTGGAGTT]ATGAGGCTGTA : 212

\* 980 \* 1000 \* 1020

TrCSa1 : -  
TrCSa2 : -  
TrCSa3 : -  
TrCSa4 : -  
TrCSa5 : TATTTCTATN : 601  
TrCSa6 : TATTTCTATCCATAGT GATCATGAAGGN : 581  
TrCSa7 : TATTTCTATCCATAGT GATCATGAAGG[GGCAACGTTAGTTCTCACACAGCTCACCTAGT] : 272

\* 1040 \* 1060 \* 1080

TrCSa1 : -  
TrCSa2 : -  
TrCSa3 : -  
TrCSa4 : -  
TrCSa5 : -  
TrCSa6 : -  
TrCSa7 : TGCTAGTTCACTATCAGATCCTTATCTGCATTGCA[GGTTAGCTGG] : 332

\* 1100 \* 1120 \* 1140

TrCSa1 : -  
TrCSa2 : -  
TrCSa3 : -  
TrCSa4 : -  
TrCSa5 : -  
TrCSa6 : -  
TrCSa7 : CCCACTGCATGGTTAGCCAATCAGGAAGTTCTACGATGGATCAGAAAGATAGTTAAGGA : 392

\* 1160 \* 1180 \* 1200

TrCSa1 : -  
TrCSa2 : -  
TrCSa3 : -  
TrCSa4 : -  
TrCSa5 : -  
TrCSa6 : -  
TrCSa7 : GTTTGGAACCTCAAACATAAGTACAGAACATTGAGCGACTACATTCAAAAAACATTGAA : 452

\* 1220 \* 1240 \* 1260

TrCSa1 : -  
TrCSa2 : -  
TrCSa3 : -  
TrCSa4 : -  
TrCSa5 : -  
TrCSa6 : -  
TrCSa7 : CAGTGGCCAGGTTGCCTGGATATGGACATGGAGTTTGCGCAATACAGACCCAAGATA : 512

\* 1280 \* 1300

TrCSa1 : -  
TrCSa2 : -  
TrCSa3 : -  
TrCSa4 : -  
TrCSa5 : -  
TrCSa6 : -  
TrCSa7 : CACTTGCCAGAGGGAGTTGCATTGAAGCATTGCCTAATGATCCAN : 559

Sequence 102 Consensus contig nucleotide sequence of TrCSb

\* 20 \* 40 \* 60  
TrCSb : CNTTTCNTTCACAGCATCCTAATCCTAATCCTAATCCTATTACTAATTACTA : 60

\* 80 \* 100 \* 120  
TrCSb : ATTACTAATTACTAGTACTAATTAGTAATACCGATCCCTTTCTGAACCCATTCAATC : 120

\* 140 \* 160 \* 180  
TrCSb : AAGNAGAAGAAGGAAAAACAAAATCCACACAAACAAACATCTTACAACAATGTCAACGAC : 180

\* 200 \* 220 \* 240  
TrCSb : AACTACTACAACCGACGAATCCAAGCTGCACGACGCTGCACGGAACCGTTGCCACCC : 240

\* 260 \* 280 \* 300  
TrCSb : CTCAGCTCACTTGCTTCCTCCACAAACCTCCGCCGCGCTCCATCCTATTCACCT : 300

\* 320 \* 340 \* 360  
TrCSb : TTCTTCTTCCTCCGGATCTCCCCACCGTCTAATGTCAAAGGAACACTCACCGTTGTTGA : 360

\* 380 \* 400 \* 420  
TrCSb : TGAACGTACCGGGAAAGTATAACCATTGAGGTCTCTCCTGATGGCACCGTTAAAGCCAA : 420

\* 440 \* 460 \* 480  
TrCSb : TGATTCAAGAAGATATCAACTGGGAAGAATGATAAGGGACTCAAACCTTATGATCCTGG : 480

\* 500 \* 520 \* 540  
TrCSb : ATATTTAACACTGCTCTGTGCGATCAACAATTCTTATATTGATGGTATGAGGGAAT : 540

\* 560 \* 580 \* 600  
TrCSb : CCTTAGATATAGAGGATACCCATTGAGGAGTTGCCGAGAAAAGCACCTTCGGAAGT : 600

\* 620 \* 640 \* 660  
TrCSb : GGCATATCTCATATTGTATGAAATTGCTTCTGCAAATCAGTTACAAGAATGGGAATT : 660

\* 680 \* 700 \* 720  
TrCSb : TGCTATATCTCAGCATTCAAGCCTTACCTCAAGGAGTTGGATCTCATACAATCAATGCC : 720

\* 740 \* 760 \* 780  
TrCSb : TCAAGATGCACATCCTATGGCGTCCTAGTGAATGCAATAAGCGCTCTGTCTGTTTCA : 780

\* 800 \* 820 \* 840  
TrCSb : TCCTGACGCAAATCCTGCTCTCAGAGGTCTTGACATCTACAACCTAAAGCAAGTGAGAGA : 840

\* 860 \* 880 \* 900  
TrCSb : CAAACAAATAGCACGGATTATTGAAAGATAACAACAATTGCTGCTGCAATTAAATCTTAG : 900

\* 920 \* 940 \* 960  
TrCSb : AATGGCAGGAAGGCCACCTGTGCTTCCATCCAACAAACTATCTTACACAGAGAACTTCCT : 960

\* 980 \* 1000 \* 1020  
TrCSb : ATACATGCTTGATTCTCTAGGCAATCGGTATATAAACCCAACCCTCAGCTAACTCGTGC : 1020

\* 1040 \* 1060 \* 1080  
TrCSb : ACTAGACATCATCTTCATCCTGCATGCAGAACATGAAATGAATTGCTCTACATCTGCTGT : 1080

\* 1100 \* 1120 \* 1140  
TrCSb : ACGACACCTTGCATCAAGCGCGTCGATGTATACACTGCTATTGCTGGAGGTGTTGGAGC : 1140

\* 1160 \* 1180 \* 1200  
TrCSb : TCTGTATGGACCTCTTCATGGTGGAGCTAATGAGGCCGCTTAAAATGCTGAGTGAAAT : 1200

\* 1220 \* 1240  
TrCSb : TGGAAGTGTGATAACATTCCAGAGTTCATTGAAGGTGTTAANN : 1244

e 103 Deduced amino acid sequence of TrCSb

*            20	*            40	*            60
TrCSb : MSTTTTTTDESKLHDAARNRLATLSAHLLPSSTTSALLHPIHLSSSSGISPPSNVKGTL		: 60
*            80	*            100	*            120
TrCSb : TVVDERTGKKYKIEVSPDGTVKANDFKKISTGKNDKGLKLYDPGYLNTPVRSTISYIDG		: 120
*            140	*            160	*            180
TrCSb : DEGILRYRGYPIEELAEKSTFPPEVAYLILYGNLPSANQLQEWEFAISQHSALPQGVLDLI		: 180
*            200	*            220	*            240
TrCSb : QSMPQDAHPMGVLVNAISALSVFHPDANPALRGLDIYNSKQVRDKQIARIIGKITTIAAA		: 240
*            260	*            280	*            300
TrCSb : INLRMAGRPPVLPNSNKLSYTENFLYMLDSLGNRSYKPNPQLTRALDIIFILHAEHEMNCS		: 300
*            320	*            340	*
TrCSb : TSAVRHLASSGVDVYTIAAGGVGALYGPLHGGANEAVLKMLSEIGSVDNIPFIEGVX		: 358

Figure 104 Nucleotide sequences of nucleic acid fragments contributing to the consensus contig sequence TrCSb

	*	20	*	40	*	60	
TrCSb1	:	CNTTCNTTCCACAGCATCTAATCCTAACCTAACCTATTA					60
TrCSb2	:	-					-
TrCSb3	:	-					-
TrCSb4	:	-					-
TrCSb5	:	-					-
TrCSb6	:	-					-
TrCSb7	:	-					-
	*	80	*	100	*	120	
TrCSb1	:	ATTACTAATTACTAGTACTAAATTAGTAATACCGATCCCTTTCTGAACCCATTCA					120
TrCSb2	:	-					-
TrCSb3	:	-					-
TrCSb4	:	-					-
TrCSb5	:	-					-
TrCSb6	:	-					-
TrCSb7	:	-					-
	*	140	*	160	*	180	
TrCSb1	:	AATTCAAAGAAGGAAAAACAAAT-CACACAAACAAACATCTTACAACAAATGTCAACGAC					179
TrCSb2	:	-GNAGNAGAAGGAAAACNC-AAAATCCACAAAC-AAAAC-TCTTACAACAAATGTCAACGAC					55
TrCSb3	:	-GNNGNAGAAGGAAAACACAAAATNCACAAAGAATAAACATCTTACAACAAATGTCAACGAC					58
TrCSb4	:	-GNAAGAGGAAAAAAC-AAAT-MCACAAAC-AACATTTAC-AACATGTC-ACGAC					50
TrCSb5	:	-GNAAGGAAAAAAC-AAAT-MC-CAAAC-AAC-TCTTAC-AACATGTC-ACGAC					45
TrCSb6	:	-					-
TrCSb7	:	-					-
	*	200	*	220	*	240	
TrCSb1	:	AACTACTACAACCGACGAATCCAAGCTGCACGACGCTGCACGGAACCGTTGGCTAACCT					239
TrCSb2	:	AACTACTACAACCGACGAATCCAAGCTGCACGACGCTGCACGGAACCGTTGGCTAACCT					115
TrCSb3	:	AACTACTACAACCGACGAATCCAAGCTGCACGACGCTGCACGGAACCGTTGGCTAACCT					118
TrCSb4	:	AACTACTACAACCGACGAATCCAAGCTGCACGACGCTGCACGGAACCGTTGGCTAACCT					110
TrCSb5	:	AACTACTACAACCGACGAATCCAAGCTGCACGACGCTGCACGGAACCGTTGGCTAACCT					105
TrCSb6	:	-					-
TrCSb7	:	-					-
	*	260	*	280	*	300	
TrCSb1	:	CTCAGCTCACTTGCTTCTCTCCACAAACTCCGCTGGCCTCTCCATCCTATTACACCT					299
TrCSb2	:	CTCAGCTCACTTGCTTCTCTCCACAAACCTCCGCCGCCCTCCATCCTATTACACCT					175
TrCSb3	:	CTCAGCTCACTTGCTTCTCTCCACAAACCTCCGCCGCCCTCCATCCTATTACACCT					178
TrCSb4	:	CTCAGCTCACTTGCTTCTCTCCACAAACCTCCGCCGCCCTCCATCCTATTACACCT					170
TrCSb5	:	CTCAGCTCACTTGCTTCTCTCCACAAACTCCGCTGGCCTCTCCATCCTATTACACCT					165
TrCSb6	:	-					-
TrCSb7	:	-					-
	*	320	*	340	*	360	
TrCSb1	:	TTCTTCTTCCTCGGGATCTCCCCACCGTCTAATGTCAAAGAACACTGACCGTTGTTGA					359
TrCSb2	:	TTCCGGCTTCTCCGGGATCTCCCCACCGTCTAATGTCAAAGAACACTGACCGTTGTTGA					235
TrCSb3	:	TTCCGGCTTCTCCGGGATCTCCCCACCGTCTAATGTCAAAGAACACTGACCGTTGTTGA					238
TrCSb4	:	TTCTTCTTCCTCCGGGATCTCCCCACCGTCTAATGTCAAAGAACACTGACCGTTGTTGA					230
TrCSb5	:	TTCTTCTTCCTCGGGATCTCCCCACCGTCTAATGTCAAAGAACACTGACCGTTGTTGA					225
TrCSb6	:	-					-
TrCSb7	:	-					-

	* 380 *	* 400 *	* 420 *	
TrCSb1 :	TGAACGTACCAGGGAAAGAAGTATACCATTGAGGTCTCCTGATGGCACCGTTAAAGCCAA		: 419	
TrCSb2 :	TGAACGTACCAGGGAAAGAAGTATAACATTGAGGTCTCACTGATGGCACCGTTAAAGCCAA		: 295	
TrCSb3 :	TGAACGTACCAGGGAAAGAAGTATAACATTGAGGTCTCACTGATGGCACCGTTAAAGCCAA		: 298	
TrCSb4 :	TGAACGTACCAGGGAAAGAAGTATACCATTGAGGTCTCCTGATGGCACCGTTAAAGCCAA		: 290	
TrCSb5 :	TGAACGTACCAGGGAAAGAAGTATACCATTGAGGTCTCCTGATGGCACCGTTAAAGCCAA		: 285	
TrCSb6 :	- - - - -		:	
TrCSb7 :	- - - - -		:	
	* 440 *	* 460 *	* 480 *	
TrCSb1 :	TGATTTCAAGAAGATATCAACTGGAAAGAATGATAAGGGCTCAAACTTATGATCCTGG		: 479	
TrCSb2 :	TGATTTCAAGAAGATATCAACTGGAAAGAATGATAAGGGACTCAAACTTATGATCCTGG		: 355	
TrCSb3 :	TGATTTCAAGAAGATATCAACTGGAAAGAATGATAAGGGACTCAAACTTATGATCCTGG		: 358	
TrCSb4 :	TGATTTCAAGAAGATATCGACTGGAAAGAATGATAAGGGACTCAAACTTATGATCCTGG		: 350	
TrCSb5 :	TGATTTCAAGAAGATATCAACTGGAAAGAATGATAAGGGCTCAAACTTATGATCCTGG		: 345	
TrCSb6 :	- - - - -		:	
TrCSb7 :	- - - - -		:	1
	* 500 *	* 520 *	* 540 *	
TrCSb1 :	ATATTTAACACTGCTCCTGTGCGATCAACAATTCTTATATTGATGGTATGAGGGAAT		: 539	
TrCSb2 :	ATATTTAACACTGCTCCTGTGCGATCAACAATTCTTATATTGATGGTATGAGGGAAT		: 415	
TrCSb3 :	ATATTTAACACTGCTCCTGTGCGATCAACAATTCTTATATTGATGGTATGAGGGAAT		: 418	
TrCSb4 :	ATATTTAACACTGCTCCTGTGCGATCAACAATTCTTATATTGATGGTATGAGGGAAT		: 410	
TrCSb5 :	ATATTTAACACTGCTCCTGTGCGATCAACAATTCTTATATTGATGGTATGAGGGAAT		: 405	
TrCSb6 :	- - - - -		:	
TrCSb7 :	- - - - -		:	
	* 560 *	* 580 *	* 600 *	
TrCSb1 :	CCTTAGATATAGAGGGATACCCCATTGAAGAGTTGCCGAGAAAAGCACCTTCGGAAAGT		: 599	
TrCSb2 :	CCTTAGATATAGAGGGATACCCCATTGAGGAGTTGCCGAGAAAAGCACCTTCGGAAAGT		: 475	
TrCSb3 :	CCTTAGATATAGAGGGATACCCCATTGAGGAGTTGCCGAGAAAAGCACCTTCGGAAAGT		: 478	
TrCSb4 :	CCTTAGATATAGAGGGATACCCCATTGAGGAGTTGCCGAGAAAAGCACCTTCGGAAAGT		: 470	
TrCSb5 :	CCTTAGATATAGAGGGATACCCCATTGAAGAGTTGCCGAGAAAAGCACCTTCGGAAAGT		: 465	
TrCSb6 :	- - - - - ATAGAGGGT - CCNATTGAGGAGTTGGCGAGAAAAGCACCTTCGGAAAGT		:	49
TrCSb7 :	- - - - -		:	
	* 620 *	* 640 *	* 660 *	
TrCSb1 :	GGCATATCTN		: 609	
TrCSb2 :	GGCATATCTCATATTGTATGAAATTGCCTTCTGCAAATCAGTTACAAGAAATGGGAATT		: 535	
TrCSb3 :	GGCATATCTCATATTGTATGAAATTGCCTTCTGCAAATCAGTTACAAGAAATGGGAATT		: 538	
TrCSb4 :	GGCATATCTCATATTGTATGAAATTGCCTTCTGCAAATCAGTTACAAGAAATGGGAATT		: 530	
TrCSb5 :	GGCATATCTCATATTGTATGAAATTGCCTTCTGCAAATCAGTTACAAGAAATGGGAATT		: 525	
TrCSb6 :	GGCATATCTCATATTGTATGAAATTGCCTTCTGCAAATCAGTTACAAGAAATGGGAATT		: 108	
TrCSb7 :	GGCATATCTCATATTGTATGAAATTGCCTTCTGCAAATCAGTTACAAGAAATGGGAATT		: 12	
	* 680 *	* 700 *	* 720 *	
TrCSb1 :	- - - - - TGCTATATCTCAGCATTCAAGCCTTACCTCAAGGAGTTTGATCTCATACAATN		:	
TrCSb2 :	TGCTATATCTCAGCATTCAAGCCTTACCTCAAGGAGTTTGATCTCATACAATCN		: 589	
TrCSb3 :	TGCTATATCTCAGCATTCAAGCCTTACCTCAAGGAGTTTGATCTCATACAATCN		: 594	
TrCSb4 :	TGCTATATCTCAGCATTCAAGCCTTACCTCAAGGAGTTTGATCTCATACAATCN		: 570	
TrCSb5 :	TGCTATATCTCAGCATTCAAGCCTTACCTCAAGGAGTTTGATCTCATACAATCAATGCC		: 585	
TrCSb6 :	GGCTATATCTCAGCATTCAAGCCTTACCTCAAGGAGTTTGATCTCATACAATCAATGCC		: 168	
TrCSb7 :	GGCTATATCTCAGCATTCAAGCCTTACCTCAAGGAGTTTGATCTCATACAATCAATGCC		: 70	

\* 740

\* 760

\* 780

TrCSb1 : -  
 TrCSb2 : -  
 TrCSb3 : -  
 TrCSb4 : -  
 TrCSb5 : TCAAGNN : 592  
 TrCSb6 : TCAATGACATCCTATGGGTGTCCTAGTGAATGCAATAAGCGCTCTTCTGTTTTCA : 228  
 TrCSb7 : TCAAGATGCACATCCTATGGCGTGCTTGTAAATGCFCTAAGCTGCTTGTCTGTTTTCA : 130

\* 800

\* 820

\* 840

TrCSb1 : -  
 TrCSb2 : -  
 TrCSb3 : -  
 TrCSb4 : -  
 TrCSb5 : -  
 TrCSb6 : TCCTGACGCCAATCCTGCTCTTACAGAGGTCTTGAATTTACGACTCAAAGGAAGTGAGAGA : 288  
 TrCSb7 : TCCTGAAATCCTGCTCTCAGAGGTCTTGAACATCTACAACCAAAGCAAGTGAGAGA : 190

\* 860

\* 880

\* 900

TrCSb1 : -  
 TrCSb2 : -  
 TrCSb3 : -  
 TrCSb4 : -  
 TrCSb5 : -  
 TrCSb6 : CAAACAAATAGCACGGATTATTGGAAAGATAACAATTGCTGCTGCAGTTATCTTAG : 348  
 TrCSb7 : CAAACAAATAGTGCGGATTATTGGAAAGATAACAACAATTGCTGCTGCAGTTATCTTAG : 250

\* 920

\* 940

\* 960

TrCSb1 : -  
 TrCSb2 : -  
 TrCSb3 : -  
 TrCSb4 : -  
 TrCSb5 : -  
 TrCSb6 : AATGGCAGGAAGGCCACCTGTGCTTCCATCCAACGAACTATCTTACACGGAGAACCTCCT : 408  
 TrCSb7 : ATGGCAGGAAGGCCACCTGTCTTCCATCCAACAACTTCTTACACAGAGAACCTCCT : 310

\* 980

\* 1000

\* 1020

TrCSb1 : -  
 TrCSb2 : -  
 TrCSb3 : -  
 TrCSb4 : -  
 TrCSb5 : -  
 TrCSb6 : ATACATGCTTGATTCTTCTAGGCAATCGGTATATAAACCAACCCCTCAGCTAACTCGTGC : 468  
 TrCSb7 : TTACATGCTTGATTCTCTGGCAATCGGTATATAAACCTAACCTCTAACTCGTGC : 370

\* 1040

\* 1060

\* 1080

TrCSb1 : -  
 TrCSb2 : -  
 TrCSb3 : -  
 TrCSb4 : -  
 TrCSb5 : -  
 TrCSb6 : ACTAGACATATCTTCATCTGCATGCAGAACATGAAATGAATTGCTCTACATCTGCTGT : 528  
 TrCSb7 : ACTGGACATCATCTTCATCTGCAGAACATGAAATGAATTGCTCTACATCTGCTGT : 430

\* 1100 \* 1120 \* 1140

TrCSb1 : - - - - -  
TrCSb2 : - - - - -  
TrCSb3 : - - - - -  
TrCSb4 : - - - - -  
TrCSb5 : - - - - -  
TrCSb6 : **CGGACACCTTGCATCAAGGGCGTGGATGTATAACTGCTATTGCTGGGG** : 579  
TrCSb7 : **ACGGCACCTTGCATCAAGGGGGTGCGATGTACACTGCTATTGCTGGAGGTGTTGGAGC** : 490

\* 1160 \* 1180 \* 1200

TrCSb1 : - - - - -  
TrCSb2 : - - - - -  
TrCSb3 : - - - - -  
TrCSb4 : - - - - -  
TrCSb5 : - - - - -  
TrCSb6 : **TCTGTATGGACCTCTTCATGGTGGAGCTAATGAGGCGGTCTAAATGCTGAGTGAAAT** : 550  
TrCSb7 : **TGGAAGTGTGATAAACATTCCAGAGTTCATTGAAGGTGTTAANN** : 594

\* 1220 \* 1240